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OM protein - protein search, using sw model

Run on: May 17, 2004, 11:10:57 ; Search time 50.3556 Seconds
(without alignments)
740.659 Million cell updates/sec

Title: US-10-010-942B-2

Perfect score: 692

Sequence: 1 MMSPAQFLFLLVLWIRETNG.....CWQGTHFPRTFGGGTKLEIK 132

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_29Jan04:*

1: geneseqp1980s:*

2: geneseqp1990s:*

3: geneseqp2000s:*

4: geneseqp2001s:*

5: geneseqp2002s:*

6: geneseqp2003as:*

7: geneseqp2003bs:*

8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query				Description
		Match	Length	DB	ID	
1	692	100.0	132	5	ABG76923	Abg76923 Mouse 3D6
2	650	93.9	135	5	ABB79729	Abb79729 Anti-Stre
3	644	93.1	239	6	ABP58274	Abp58274 Humanised
4	641	92.6	132	2	AAR12361	Aar12361 Light (ka
5	640	92.5	132	5	ABG76925	Abg76925 Humanised
6	639	92.3	131	2	AAR12239	Aar12239 Mouse MAb
7	636	91.9	132	6	ABG74244	Abg74244 Mouse ant
8	630	91.0	132	5	ABG76931	Abg76931 Humanised
9	628	90.8	132	2	AAR24712	Aar24712 Sequence

10	606	87.6	142	4	AAE07032	Aae07032 Murine an
11	595	86.0	239	2	AAR24811	Aar24811 Sequence
12	589	85.1	239	7	ADD47025	Add47025 Rat Prote
13	571	82.5	113	4	AAE03751	Aae03751 Murine PS
14	571	82.5	218	4	AAE03756	Aae03756 Chimeric
15	562	81.2	353	2	AY06273	Aay06273 Anti Fc a
16	560	80.9	112	4	AAE06946	Aae06946 Murine 1D
17	560	80.9	112	4	AAU09918	Aau09918 Murine mA
18	560	80.9	112	5	ABG75527	Abg75527 Mouse mAb
19	560	80.9	112	7	ABR61865	Abr61865 Mouse MAb
20	560	80.9	257	3	AAB09777	Aab09777 Antiviral
21	559	80.8	112	2	AY52765	Aay52765 Anti-tiss
22	559	80.8	112	2	AY52766	Aay52766 Anti-tiss
23	556	80.3	112	4	AAE06991	Aae06991 Human kap
24	555	80.2	112	5	AAO14971	Aao14971 Mouse lig
25	550	79.5	243	2	AAW60769	Aaw60769 Single ch
26	548	79.2	112	2	AAW48248	Aaw48248 A77 anti-
27	548	79.2	112	4	AAB74621	Aab74621 A77 anti-
28	548	79.2	112	4	AAE08554	Aae08554 Murine A7
29	548	79.2	535	2	AAW28491	Aaw28491 Human p53
30	548	79.2	535	2	AAW28492	Aaw28492 Human p53
31	547	79.0	162	7	ADE06760	Ade06760 D13 light
32	546	78.9	112	7	ABR62960	Abr62960 Monoclonal
33	543	78.5	113	6	ABP58270	Abp58270 Humanised
34	543	78.5	219	6	ABP58272	Abp58272 Humanised
35	539	77.9	272	2	AAW43913	Aaw43913 Mus musculus
36	538	77.7	112	4	AAE06951	Aae06951 Humanised
37	538	77.7	112	4	AAU09923	Aau09923 Humanised
38	538	77.7	112	5	ABG75532	Abg75532 Humanised
39	538	77.7	112	6	ABB99636	Abb99636 2A2 monoc
40	537	77.6	132	2	AAW79225	Aaw79225 Humanised
41	537	77.6	132	2	AAW56349	Aaw56349 Humanised
42	537	77.6	132	2	AYY30186	Aay30186 Sequence
43	536	77.5	113	7	ADD05270	Add05270 Female mouse
44	535	77.3	272	2	AAW00557	Aaw00557 Nematode
45	533	77.0	112	4	AAE06952	Aae06952 Humanised

ALIGNMENTS

RESULT 1
 ABG76923
 ID ABG76923 standard; protein; 132 AA.
 XX
 AC ABG76923;
 XX
 DT 05-NOV-2002 (first entry)
 XX
 DE Mouse 3D6 VL protein.
 XX
 KW Mouse; humanized; immunoglobulin; Ig; light chain; LC; heavy chain; HC;
 KW variable region complementarity determining region; 3D6; 10D5;
 KW variable framework region; amyloidogenic disease; Alzheimer's disease;
 KW amyloid deposit; variable light chain; VL; variable heavy chain; VH;
 KW nootropic; neuroprotective; inhibitor of beta amyloid accumulation;
 KW Abeta.

XX
OS Mus musculus.
XX
PN WO200246237-A2.
XX
PD 13-JUN-2002.
XX
PF 06-DEC-2001; 2001WO-US046587.
XX
PR 06-DEC-2000; 2000US-0251892P.
XX
PA (NEUR-) NEURALAB LTD.
PA (AMHP) WYETH.
XX
PI Basi G, Saldanha J, Yednock T;
XX
DR WPI; 2002-519658/55.
DR N-PSDB; ABS59426.
XX
PT Novel light/heavy chain of humanized immunoglobulin for treating
PT amyloidogenic disease, has 3D6/10D5 variable region complementarity
PT determining regions and variable framework region from human acceptor
PT immunoglobulin.

XX
PS Claim 67; Fig 1; 171pp; English.
XX
CC The present invention relates to new humanized immunoglobulin (Ig) light
CC chain (LC) or heavy chain (HC) comprising variable region complementarity
CC determining regions from 3D6/10D5 Ig LC or HC variable region sequence,
CC and variable framework region from human acceptor Ig LC or HC sequence.
CC The invention is useful for preventing or treating an amyloidogenic
CC disease or Alzheimer's disease in a patient. The invention is also useful
CC for in vivo imaging amyloid deposits in a patient. The present amino acid
CC sequence represents a mouse 3D6/10D5 variable light (VL) chain or
CC variable heavy (VH) chain protein of the invention

XX
SQ Sequence 132 AA;

Query Match 100.0%; Score 692; DB 5; Length 132;
Best Local Similarity 100.0%; Pred. No. 4.7e-55;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MMSPAQFLFLLVLWIRETNGYVVMTQTPLTLSVTIGQPASISCKSSQSLLSDGKTYLNW 60
Db |||||||
Qy 61 LLQRPGQSPKRЛИYLVSKLDGVPDRFTGSGSGTDFTLKISRIEAEDLGLYYCWQGTHFP 120
Db 61 LLQRPGQSPKRЛИYLVSKLDGVPDRFTGSGSGTDFTLKISRIEAEDLGLYYCWQGTHFP 120
Qy 121 RTFGGGTKLEIK 132
Db 121 RTFGGGTKLEIK 132

RESULT 2
ABB79729

ID ABB79729 standard; protein; 135 AA.
XX
AC ABB79729;
XX
DT 29-OCT-2002 (first entry)
XX
DE Anti-Streptococcus mutans surface antigen MAb SWLA3 VL.
XX
KW Streptococcus mutans; monoclonal antibody; MAb; mouse; chimeric antibody;
KW antibody; anticaries; transgenic plant; transgenic animal; caries;
KW immunotherapy; therapy.
XX
OS Mus musculus.
XX
PN US2002068066-A1.
XX
PD 06-JUN-2002.
XX
PF 15-JUN-2001; 2001US-00881823.
XX
PR 20-AUG-1999; 99US-00378577.
XX
PA (SHIW/) SHI W.
PA (MORR/) MORRISON S L.
PA (TRIN/) TRINH K.
PA (WIMS/) WIMS L.
PA (CHEN/) CHEN L.
PA (ANDE/) ANDERSON M H.
XX
PI Shi W, Morrison SL, Trinh K, Wims L, Chen L, Anderson MH;
XX
DR WPI; 2002-565838/60.
DR N-PSDB; ABN84610.
XX
PT Treatment and prevention of dental caries in mammals, in particular
PT humans by orally administering genetically engineered or purified
PT antibodies that bind to surface antigens of carcinogenic organisms.
XX
PS Claim 13; Fig 3A; 30pp; English.
XX
CC The present sequence is the protein sequence of the light chain variable
CC region (VL) of the murine monoclonal antibody SWLA3 (IgG), which binds
CC specifically to the surface antigens of cariogenic type c Streptococcus
CC mutans (ATCC 25175). The monoclonal antibody is produced by SWLA3 (ATCC
CC HB 12558) hybridoma cells. In an example from the invention, chimeric
CC monoclonal antibody TEFE was produced comprising SWLA3 variable regions
CC and human antibody constant regions. Such chimeric monoclonal antibodies
CC can be used to prevent or treat dental caries in humans. The antibodies
CC engage the effector apparatus of the human immune system when they bind
CC cariogenic organisms, resulting in their destruction. The chimeric
CC antibodies may be produced in edible plants, in transgenic animals, or in
CC chicken eggs for oral ingestion
XX
SQ Sequence 135 AA;

Query Match 93.9%; Score 650; DB 5; Length 135;
Best Local Similarity 93.2%; Pred. No. 3.1e-51;

Matches	123;	Conservative	5;	Mismatches	4;	Indels	0;	Gaps	0;
Qy	1 MMSPAQFLFLLVLWIRETNGYVVMTQTPLTLSVTIGQPASISCKSSQSLLSDGKTYLNW 60 : :								
Db	1 MMSPAQFLFLLVLWIRETNGDVVMTQTPLTLSVTIGQPASISCKSSQSLLDRDGRTYLSW 60								
Qy	61 LLQRPGQSPKRЛИYLVSKLDGVPDRFTGSGSGTDFTLKISRVEAEDLGLYYCWQGTHFP 120 : : : :								
Db	61 LLQRPGQSPKRЛИYLVSKLDGVPDRFTGSGSGTDFTLKISRVEAEDLGLYYCWQGTHFP 120								
Qy	121 RTFGGGTKLEIK 132 :								
Db	121 LTFGAGTKLELK 132								

RESULT 3
 ABP58274
 ID ABP58274 standard; protein; 239 AA.
 XX
 AC ABP58274;
 XX
 DT 23-OCT-2003 (revised)
 DT 31-MAR-2003 (first entry)
 XX
 DE Humanised 3D6 antibody light chain.
 XX
 KW Monoclonal antibody; 3D6; complementarity determining region; CDR; mouse;
 KW human; humanised antibody; antibody; Alzheimer's disease;
 KW Down's syndrome; cerebral amyloid angiopathy; neuroprotective; nootropic.
 XX
 OS Mus sp.
 OS Homo sapiens.
 OS Chimeric.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1. .20
 FT /label= Signal_peptide
 FT Protein 21. .239
 FT /label= Mature_peptide
 FT /note= "the mature light chain is claimed in Claim 5"
 FT Region 21. .133
 FT /note= "light chain variable region, claimed in Claim 4"
 FT Region 44. .59
 FT /note= "CDR1"
 FT Region 75. .81
 FT /note= "CDR2"
 FT Region 114. .122
 FT /note= "CDR3"
 XX
 PN WO200288306-A2.
 XX
 PD 07-NOV-2002.
 XX
 PF 26-APR-2002; 2002WO-US011853.
 XX
 PR 30-APR-2001; 2001US-0287539P.
 XX

PA (ELIL) LILLY & CO ELI.
XX
PI Tsurushita N, Vasquez M;
XX
DR WPI; 2003-183835/18.
DR N-PSDB; ABZ24632, ABZ24634.
XX
PT New humanized forms of mouse 3D6 antibodies, useful for treating Down's
PT syndrome, (pre-)clinical Alzheimer's disease or (pre-)clinical cerebral
PT amyloid angiopathy, or for inhibiting formation of or reducing Abeta
PT plaque in the brain.
XX
PS Disclosure; Page 12-13; 54pp; English.
XX
CC The present sequence is that of a preferred light chain of a humanised
CC antibody of the present invention. In the variable region of this
CC sequence, the complementarity determining regions (CDRs) originate from
CC murine monoclonal antibody 3D6 and the framework region from human
CC germline Vk segment DPK19 and J segment Jk4. Novel humanised antibodies
CC of the invention have CDRs from 3D6 and human framework sequences. These
CC humanised antibodies have binding affinities (affinity and epitope
CC location) approximately the same as those of the mouse 3D6 antibody. The
CC invention includes antibodies, single chain antibodies, and their
CC fragments, as well as nucleotide sequences, vectors, transformed host
CC cells, and methods of using the humanised antibody to treat, prevent,
CC alleviate, reverse or otherwise ameliorate symptoms and/or pathology
CC associated with Down's syndrome, (pre-)clinical Alzheimer's disease or
CC (pre-)clinical cerebral amyloid angiopathy, and to inhibit formation or
CC reduce Abeta plaque in the brain. (Updated on 23-OCT-2003 to standardise
CC OS field)
XX
SQ Sequence 239 AA;

```

Query Match         93.1%;  Score 644;  DB 6;  Length 239;
Best Local Similarity  90.9%;  Pred. No. 2.1e-50;
Matches 120;  Conservative  9;  Mismatches  3;  Indels  0;  Gaps  0;

Y      1 MMSPAQFLFLLVLWIRETNGYVVMTQTPLTLSVTIGQPASISCKSSQSLLSDGKTYLNW 60
|:|||||||:|||||||:|||||:|||:| ||:|||||||:|||||||:|||||||:|||||||:|
b      1 MMSPAQFLFLLVLWIRETNGDVVMTQSPLSLPVTLGQPASISCKSSQSLLSDGKTYLNW 60

Y      61 LLQRPGQSPKRЛИYLVSKLDGVPDRFTGSGSGTDFTLKISRRIEAEDLGLYYCWQGTHFP 120
|:|||||||:|||||||:|||||||:|||||||:|||||||:|||||||:|||||||:|||||||:|
b      61 LQQRPGQSPRRLIYLVSKLDGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCWQGTHFP 120

Y      121 RTFGGGTKLEIK 132
|:|||||||:|||
b      121 RTFGGGTKVEIK 132

```

RESULT 4
AAR12361
ID AAR12361 standard; protein; 132 AA.
XX
AC AAR12361;
XX
DT 25-MAR-2003 (revised)

DT 15-AUG-1991 (first entry)
XX
DE Light (kappa) chain variable region of murine 4D12 immunoglobulin.
XX
KW Chimeric antibodies; immunoconjugates; HIV; AIDS.
XX
OS Mus musculus.
XX
PN WO9107493-A.
XX
PD 30-MAY-1991.
XX
PF 13-NOV-1989; 89US-00433730.
XX
PR 13-NOV-1989; 89US-00433730.
XX
PA (XOMA) XOMA CORP.
PA (GREC) GREEN CROSS CORP.
XX
PI Better MD, Horwitz AH, Ghoshdasti P, Robinson R;
XX
DR WPI; 1991-178105/24.
DR N-PSDB; AAQ12063.
XX
PT New chimeric mouse-human antibodies - used to detect, kill and remove HIV
PT -1 antigen from sample.
XX
PS Disclosure; Fig 18; 107pp; English.
XX
CC This is the light (kappa) - chain variable (V) region of a mouse
CC monoclonal antibody (MAb), 4D12, and is specific for an HIV-1 viral
CC antigen. It is used in the construction of a chimeric MAb comprising
CC heavy and light chains having murine V regions and human C regions. The
CC chimeric MAbs are more effective than murine MAb 4D12 since they have an
CC increased compatibility in humans. The heavy and light chain V-regions
CC are joined by manipulating their respective joining (J) regions, to
CC generate restriction enzyme recognition sites. The chimeric MAbs can be
CC used as immunoconjugates, in association with e.g. toxins for HIV
CC treatment. They can also be used in diagnosis of HIV. See also AAQ12056-
CC 62. (Updated on 25-MAR-2003 to correct PA field.) (Updated on 25-MAR-2003
CC to correct PI field.) (Updated on 25-MAR-2003 to correct DR field.)
XX
SQ Sequence 132 AA;

Query Match 92.6%; Score 641; DB 2; Length 132;
Best Local Similarity 90.9%; Pred. No. 2e-50;
Matches 120; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

Qy 1 MMSPAQFLFLLVLWIRETNGYVVMTQTPLTLSVTIGQPASISCKSSQSLLSDGKTYLNW 60
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| :|||
Db 1 MMSPAQFLFLLVLWIRETNGDVVMTQTPLTLSVTIGQPASFCKSSQSLLSDGKTFLNW 60

Qy 61 LLQRPGQSPKRLLIYLVSKLDSGVDRFTGSGSGTDFTLKISRVEAEDLGLYYCWQGTHFP 120
||| ||| ||| :||| ||| ||| ||| ||| ||| ||| :||| ||| :|||
Db 61 FLQRPGQSPKRLLIYLVSKLDSGVDRFTGSGSGTDFTLKISRVEAEDLGVYYCWQGSHFP 120

Qy 121 RTFGGGTKLEIK 132

||| |||||::

Db 121 ITFGAGTKLELR 132

RESULT 5

ABG76925

ID ABG76925 standard; protein; 132 AA.

XX

AC ABG76925;

XX

DT 05-NOV-2002 (first entry)

XX

DE Humanised 3D6 light chain variable region #1.

XX

KW Mouse; humanized; immunoglobulin; Ig; light chain; LC; heavy chain; HC;
KW variable region complementarity determining region; 3D6; 10D5;
KW variable framework region; amyloidogenic disease; Alzheimer's disease;
KW amyloid deposit; variable light chain; VL; variable heavy chain; VH;
KW nootropic; neuroprotective; inhibitor of beta amyloid accumulation;
KW Abeta.

XX

OS Homo sapiens.

OS Mus musculus.

OS Synthetic.

XX

PN WO200246237-A2.

XX

PD 13-JUN-2002.

XX

PF 06-DEC-2001; 2001WO-US046587.

XX

PR 06-DEC-2000; 2000US-0251892P.

XX

PA (NEUR-) NEURALAB LTD.

PA (AMHP) WYETH.

XX

PI Basi G, Saldanha J, Yednock T;

XX

DR WPI; 2002-519658/55.

XX

PT Novel light/heavy chain of humanized immunoglobulin for treating
PT amyloidogenic disease, has 3D6/10D5 variable region complementarity
PT determining regions and variable framework region from human acceptor
PT immunoglobulin.

XX

PS Claim 54; Page 154; 171pp; English.

XX

CC The present invention relates to new humanized immunoglobulin (Ig) light
CC chain (LC) or heavy chain (HC) comprising variable region complementarity
CC determining regions from 3D6/10D5 Ig LC or HC variable region sequence,
CC and variable framework region from human acceptor Ig LC or HC sequence.
CC The invention is useful for preventing or treating an amyloidogenic
CC disease or Alzheimer's disease in a patient. The invention is also useful
CC for in vivo imaging amyloid deposits in a patient. The present amino acid
CC sequence represents a humanized 3D6 variable light (VL) chain or variable
CC heavy (VH) chain protein of the invention

XX

SQ Sequence 132 AA;

Query Match 92.5%; Score 640; DB 5; Length 132;
Best Local Similarity 90.2%; Pred. No. 2.5e-50;
Matches 119; Conservative 10; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MMSPAQFLFLLVLWIRETNGYVVMTQTPPLTLSVTIGQPASISCKSSQSLLSDGKTYLNW 60
|||:|||||:|||||:|||||:|||||:|||||:
Db 1 MMSPAQFLFLLVLWIRETNGYVVMTQSPLSLPVTPGEPASISCKSSQSLLSDGKTYLNW 60

Qy 61 LLQRPGQSPKRЛИYLVSKLDGVPDRFTGSGSGTDFTLKISRVEAEDLGLYYCWQGTHFP 120
|||:|||||:
Db 61 LLQKPGQSPQRLIYLVSKLDGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCWQGTHFP 120

Qy 121 RTFGGGTKLEIK 132
|||| |||:
Db 121 RTFGQGTKVEIK 132

RESULT 6

AAR12239

ID AAR12239 standard; protein; 131 AA.

XX

AC AAR12239;

XX

DT 25-MAR-2003 (revised)

DT 19-AUG-1991 (first entry)

XX

DE Mouse MAb 4D12 L chain V region.

XX

KW HIV-1; chimera.

XX

OS Mus sp.

XX

PN WO9107494-A.

XX

PD 30-MAY-1991.

XX

PF 13-NOV-1989; 89US-00433703.

XX

PR 13-NOV-1989; 89US-00433703.

XX

PA (XOMA) XOMA CORP.

PA (GREC) GREEN CROSS CORP.

PA (ZOMA-) ZOMA CORP.

XX

PI Better MD, Horwitz AH, Ghoshdasti P, Robinson RR;

XX

DR WPI; 1991-178106/24.

DR N-PSDB; AAQ12019.

XX

PT New chimeric mouse human antibodies - used in treatment, diagnosis and

PT prophylaxis of HIV infections.

XX

PS Disclosure; Fig 18; 108pp; English.

XX

CC The mouse VL gene product may be used to produce chimeric mouse- human

CC Abs against HIV-1 comprising human Ig constant regions and murine
CC variable regions. These novel sequence are useful in treatment, diagnosis
CC and prophylaxis of HIV infections, and may be produced by a bacterial,
CC yeast or mammalian expression system. (Updated on 25-MAR-2003 to correct
CC PA field.) (Updated on 25-MAR-2003 to correct PI field.)
XX

SQ Sequence 131 AA;

Query Match 92.3%; Score 639; DB 2; Length 131;
Best Local Similarity 91.6%; Pred. No. 3e-50;
Matches 120; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

Qy 1 MMSPAQFLFLLVLWIRETNGYVVMTQTPLTLSVTIGQPASISCKSSQSLLSDGKTYLNW 60
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| :|||

Db 1 MMSPAQFLFLLVLWIRETNGDVVMTQTPLTLSVTIGQPASFCKSSQSLLSDGKTFLNW 60

Qy 61 LLQRPGQSPKRЛИYLVSKLDGVPDRFTGSGSGTDFTLKISRVEAEDLGLYYCWQGTHFP 120
||| ||| ||| :||| ||| ||| ||| ||| ||| ||| ||| :||| ||| :||| ||| :|||

Db 61 FLQRPGQSPKRLLYLVSKLDGVPDRFTGSGSGTDFTLKISRVEAEDLGVYYCWQGSHFP 120

Qy 121 RTFGGGTKLEI 131
||| ||| :|||

Db 121 ITFGAGTKLEL 131

RESULT 7

ABG74244

ID ABG74244 standard; protein; 132 AA.

XX

AC ABG74244;

XX

DT 22-APR-2003 (first entry)

XX

DE Mouse antibody 3D8 light chain variable region.

XX

KW T-cell receptor; cytostatic; dermatological; neuroprotective;
KW immunostimulant; GD3; ganglioside antigen; MB3.6; PSMA; tumour; 3D8; 4D4;
KW 3E11; prostate-specific membrane antigen; zeta signalling chain;
KW CD8alpha hinge; cancer; melanoma; neuroendocrine tumour; prostate cancer;
KW small cell lung cancer; light chain variable region; mouse.

XX

OS Mus sp.

XX

PN US2002132983-A1.

XX

PD 19-SEP-2002.

XX

PF 10-DEC-2001; 2001US-00006773.

XX

PR 30-NOV-2000; 2000US-0250087P.

PR 30-NOV-2000; 2000US-0250089P.

XX

PA (JUNG/) JUNGHANS R P.

XX

PI Junghans RP;

XX

DR WPI; 2003-208946/20.

DR N-PSDB; ABX16570.
XX
PT New chimeric molecule useful in treating patients with disorders, such as
PT melanoma, neuroendocrine disorders, prostate and small cell lung cancer
PT comprises GD3 and/or PSMA binding domains of antibody.
XX
PS Disclosure; Page 13; 35pp; English.
XX
CC The invention relates to a chimaeric molecule comprising the GD3
CC (ganglioside antigen) binding domain of antibody MB3.6, with any of 3
CC variable gene sequences, or the PSMA (prostate-specific membrane antigen)
CC binding domain of antibody 3D8, 4D4 and 3E11, with variable gene
CC sequences, the zeta signalling chain of the T cell receptor and an
CC intervening CD8alpha hinge in which cysteine residues have been mutated.
CC The chimaeric molecules expressed in T cells or NK cells or other
CC effector cells are useful in treating patients with cancers expressing
CC the GD3 (MB3.6 derivatives) or PSMA antigen (3D8, 4D4, 3E11 derivatives),
CC and/or together with each other or with heterologous constructs to engage
CC additional stimulatory and functional properties of the effector cells to
CC enhance the antitumour therapeutic efficacy (claimed). They are
CC particularly useful in disorders including melanoma, neuroendocrine
CC tumours and prostate and small cell lung cancer. The present sequence
CC represents the mouse antibody 3D8 light chain variable region
XX
SQ Sequence 132 AA;

Query Match 91.9%; Score 636; DB 6; Length 132;
Best Local Similarity 93.9%; Pred. No. 5.7e-50;
Matches 123; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 2 MSPAQFLFLLVLWIRETNGYVVMTQTPLTSVTIGQPASISCKSSQSLLSDGKTYLNWL 61
Db 1 MSPAQFLFLLVLWIQETNGDVVMTQTPLTSVTIGQPASISCKSSQSLLYSNGKTYLNWL 60

Qy 62 LQRPGQSPKRЛИYLVSKLDGSVPDRFTGSGSGTDFTLKISRIEAEDLGLYYCWQGTHFPR 121
Db 61 LQRPGQSPKRЛИYLVSKLDGSVPDRFTGSGSGTDFTLKISRVEAEDLGVYYCVQGTHFPH 120

Qy 122 TFGGGTKLEIK 132
Db 121 TFGGGTKLEIK 131

RESULT 8
ABG76931
ID ABG76931 standard; protein; 132 AA.
XX
AC ABG76931;
XX
DT 05-NOV-2002 (first entry)
XX
DE Humanised 3D6 light chain variable region #2.
XX
KW Mouse; humanized; immunoglobulin; Ig; light chain; LC; heavy chain; HC;
KW variable region complementarity determining region; 3D6; 10D5;
KW variable framework region; amyloidogenic disease; Alzheimer's disease;
KW amyloid deposit; variable light chain; VL; variable heavy chain; VH;

KW nootropic; neuroprotective; inhibitor of beta amyloid accumulation;
KW Abeta.
XX
OS Homo sapiens.
OS Mus musculus.
OS Synthetic.
XX
PN WO200246237-A2.
XX
PD 13-JUN-2002.
XX
PF 06-DEC-2001; 2001WO-US046587.
XX
PR 06-DEC-2000; 2000US-0251892P.
XX
PA (NEUR-) NEURALAB LTD.
PA (AMHP) WYETH.
XX
PI Basi G, Saldanha J, Yednock T;
XX
DR WPI; 2002-519658/55.
XX
PT Novel light/heavy chain of humanized immunoglobulin for treating
PT amyloidogenic disease, has 3D6/10D5 variable region complementarity
PT determining regions and variable framework region from human acceptor
PT immunoglobulin.
XX
PS Claim 55; Page 157; 171pp; English.
XX
CC The present invention relates to new humanized immunoglobulin (Ig) light
CC chain (LC) or heavy chain (HC) comprising variable region complementarity
CC determining regions from 3D6/10D5 Ig LC or HC variable region sequence,
CC and variable framework region from human acceptor Ig LC or HC sequence.
CC The invention is useful for preventing or treating an amyloidogenic
CC disease or Alzheimer's disease in a patient. The invention is also useful
CC for in vivo imaging amyloid deposits in a patient. The present amino acid
CC sequence represents a humanized 3D6 variable light (VL) chain or variable
CC heavy (VH) chain protein of the invention
XX
SQ Sequence 132 AA;

Query Match 91.0%; Score 630; DB 5; Length 132;
Best Local Similarity 89.4%; Pred. No. 2e-49;
Matches 118; Conservative 10; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MMSPAQFLFLLVLWIRETNGYVVMTQTPLTLSVTIGQPASISCKSSQSLLSDGKTYLNW 60
Db 1 MMSPAQFLFLLVLWIRETNGDVVMTQSPLSLPVTPGEPASISCKSSQSLLSDGKTYLNW 60

Qy 61 LLQRPGQSPKRLIYLVSKLDSGPDRFTGSGSGTDFTLKISREREAEDLGLYYCWQGTHFP 120
Db 61 LLQKPGQSPQRRIYLVSKLDSGPDRFTGSGSGTDFTLKISRVEAEDVGVYYCWQGTHFP 120

Qy 121 RTFGGGTKLEIK 132
Db 121 RTFGQGTKVEIK 132

RESULT 9
AAR24712
ID AAR24712 standard; protein; 132 AA.
XX
AC AAR24712;
XX
DT 25-MAR-2003 (revised)
DT 28-DEC-1992 (first entry)
XX
DE Sequence encoded by the genomic FIB1-11 kappa chain variable (VFK) gene.
XX
KW Chimeric monoclonal antibody; anti-fibrin antibody; PCR;
KW antithrombotic agent; myocardial infarction therapy.
XX
OS Mus musculus.
XX
FH Key Location/Qualifiers
FT Peptide 1. .20
FT /label= leader
FT Region 21. .43
FT /label= Framework Region (FR) 1
FT Region 44. .59
FT /label= complementarity determining region(CDR)1
FT Region 60. .74
FT /label= FR-2
FT Region 75. .81
FT /label= CDR-2
FT Region 82. .112
FT /label= FR-3
FT Region 113. .122
FT /label= CDR-3
FT Region 123. .132
FT /label= FR-4
XX
PN EP491351-A2.
XX
PD 24-JUN-1992.
XX
PF 17-DEC-1991; 91EP-00121591.
XX
PR 18-DEC-1990; 90JP-00413829.
PR 11-NOV-1991; 91JP-00294464.
XX
PA (TAKE) TAKEDA CHEM IND LTD.
XX
PI Iwasa S, Tada H, Watanabe T;
XX
DR WPI; 1992-209528/26.
DR N-PSDB; AAQ25665.
XX
PT Chimeric monoclonal antibodies - contain anti-human fibrin antibody light
PT and heavy chain variable and constant for treating thrombotic conditions
PT e.g. myocardial infarction.
XX
PS Example; Fig 1; 87pp; English.
XX

FT Region 18. .130
FT /label= Variable_region
FT Region 131. .142
FT /label= Constant_region
XX
PN WO200157226-A1.
XX
PD 09-AUG-2001.
XX
PF 02-FEB-2001; 2001WO-US003537.
XX
PR 03-FEB-2000; 2000US-00497625.
XX
PA (MILL-) MILLENNIUM PHARM INC.
XX
PI Larosa GJ, Horvath C, Newman W, Jones ST, O'brien S, O'keefe T;
XX
DR WPI; 2001-488888/53.
DR N-PSDB; AAD13177.
XX
PT Humanized immunoglobulin for treating a CC-chemokine receptor 2-mediated disorder in a patient, comprises a binding specificity for CCR2, and a non-human antigen binding region and human immunoglobulin.
XX
PS Disclosure; Fig 22; 183pp; English.
XX
CC The patent discloses a humanised antibody or its antigen-binding fragment, having binding specificity for CC-chemokine receptor 2 (CCR2), comprising an antigen binding region of non-human origin and at least a portion of an immunoglobulin of human origin. The humanised antibodies are useful for inhibiting the interaction of a cell expressing CCR2. They are useful for inhibiting or treating HIV infection. The proteins of the invention are useful for inhibiting leukocyte trafficking, for treating CCR2-mediated disorders such as inflammatory disorder, autoimmune disorders such as rheumatoid arthritis and multiple sclerosis, atherosclerosis and atherosclerosis, and for inhibiting restenosis. They are useful in therapy or diagnosis, and in the manufacture of a medicament for treating CCR-2 mediated disease. They are also useful for treating allergy, anaphylaxis, malignancy, chronic and acute inflammation, histamine and IgE- mediated allergic reaction, shock, stenosis, allograft rejection, fibrotic disease, asthma, inflammatory glomerulopathies, acquired immune deficiency syndrome (AIDS), restenosis associated with vascular intervention, including angioplasty and/or stent placement in a mammal. Humanised antibodies are also useful for inhibiting narrowing of the lumen of a vessel in a mammal, and inhibiting neointimal hyperplasia of a vessel in a mammal, preferably associated with vascular intervention. The present sequence is murine antibody 1D9 kappa light chain variable region
XX
SQ Sequence 142 AA;

Query Match 87.6%; Score 606; DB 4; Length 142;
Best Local Similarity 93.5%; Pred. No. 3.2e-47;
Matches 115; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 10 LLVLWIRETNGYVVMQTPLTLSVTIGQPASISCKSSQSLLSDGKTYLNWLLQRPGQSP 69
||||||| | |||||:| |||||:| |||||:| |||||:|

Db 7 LLVLWIRETIGDVVMTQTPLTLSVTGHPASISCKSSQSLLSDGKTFLNWLLQRPGQSP 66
Qy 70 KRLIYLVSKLDGVPDFRTGSAGTDFTLKISRTEAEDLGLYYCWQGTHFPRTFGGGTKL 129
||| ||| ||| ||| ||| ||| :||| :||| :||| ||| |||
Db 67 KRLIYLVSKLDGVPDFRTGSAGTDFTLKISRVEAEDLGVYYCWQGTHFPYTFGGGTKL 126
Qy 130 EIK 132
|||
Db 127 EIK 129

RESULT 11
AAR24811
ID AAR24811 standard; protein; 239 AA.
XX
AC AAR24811;
XX
DT 25-MAR-2003 (revised)
DT 28-DEC-1992 (first entry)
XX
DE Sequence encoded by the chimeric kappa chain cDNA (lgkv) contained in
DE pTB1427.
XX
KW Chimeric monoclonal antibody; anti-fibrin antibody; primer;
KW antithrombotic agent; myocardial infarction therapy.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Peptide 1. .20
FT /label= leader
FT Region 21. .133
FT /label= V-kappa
FT Misc-difference 130
FT /note= "Alternatively = Glu"
FT Region 134. .239
FT /label= C-kappa
XX
PN EP491351-A2.
XX
PD 24-JUN-1992.
XX
PF 17-DEC-1991; 91EP-00121591.
XX
PR 18-DEC-1990; 90JP-00413829.
PR 11-NOV-1991; 91JP-00294464.
XX
PA (TAKE) TAKEDA CHEM IND LTD.
XX
PI Iwasa S, Tada H, Watanabe T;
XX
DR WPI; 1992-209528/26.
DR N-PSDB; AAQ25691.
XX
PT Chimeric monoclonal antibodies - contain anti-human fibrin antibody light
PT and heavy chain variable and constant for treating thrombotic conditions
PT e.g. myocardial infarction.

XX
PS Example; Fig 9; 87pp; English.
XX
CC Poly(A)+ RNA was prep'd. from the anti-fibrin chimeric Ab-producing
CC transformant FIB1-H01/X63 and used as a template to clone human C-kappa
CC cDNA, using the oligo-dT (Pharmacia) primer as a primer for first strand
CC cDNA synthesis and the 3'E-kappa and 5'C-kappa primers for the PCR. An
CC amplified DNA fragment of about 0.33kb was isolated and used to create a
CC C-kappa cDNA contg. vector, pTB1394. Using the same technique, with the
CC 3'E-kappa primer as a primer for first strand synthesis and the 5'L-kappa
CC and 3'C-kappa primers for the PCR, an anti-fibrin V-kappa (V-kappa-v)
CC cDNA was amplified. Furthermore, using the 3'E-kappa primer for first
CC strand synthesis and the 5'mV-kappa and 3'mV-kappa primers for the PCR, an
CC anti-fibrin V-kappa cDNA (V-kappa-FIB) was amplified. In addition, a
CC leader sequence cDNA (L-kappa) was amplified using the 3'C-kappa as a
CC primer for first strand synthesis and the 5'S-kappa and 3'L- kappa
CC primers for the PCR. The amplified gene fragments (L-kappa: V-kappa-v: V-
CC kappa-FIB) were isolated and used to construct respectively plasmids
CC pTB1391, pTB1392, and pTB1393. L-kappa, V- kappa and C-kappa were joined
CC together to give a plasmid, pTB1427, contg. the whole length of the
CC chimeric kappa chain cDNA. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 239 AA;

Query Match 86.0%; Score 595; DB 2; Length 239;
Best Local Similarity 85.6%; Pred. No. 5.7e-46;
Matches 113; Conservative 7; Mismatches 12; Indels 0; Gaps 0;

Qy 1 MMSPAQFLFLLVLWIRETNGYVVMTQTPLTLSVTIGQPASISCKSSQSLLSDGKTYLNW 60
||| ||| ||| ||| ||| ||| | : : ||| ||| ||| ||| ||| : ||| ||| ||| |||
Db 1 MMSPAQFLFLLVLWIRETRGDIQLAQTPLTFSVTIGQPAFISCTSSQTLSDGKTYLNW 60

Qy 61 LLQRPGQSPKRЛИYLVSKLDGVPDRFTGSGSGTDFTLKISRIEADLGLYYCWQGTHFP 120
||| ||| : ||| ||| ||| ||| ||| ||| ||| ||| : ||| : ||| ||| : ||| ||| |||
Db 61 LLQRPGQSPRRLIYLVSKLYSGVPDRFTGSGSGTAFTLKINRVEAEDLGVYYCWQGIHFP 120

Qy 121 RTFGGGTKLEIK 132
||| ||| ||| |||
Db 121 YTFGGGTKLVIK 132

RESULT 12
ADD47025
ID ADD47025 standard; protein; 239 AA.
XX
AC ADD47025;
XX
DT 29-JAN-2004 (first entry)
XX
DE Rat Protein L22655, SEQ ID NO 12711.
XX
KW Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
KW chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
XX
OS Rattus norvegicus.
XX
PN WO2003016475-A2.

XX
PD 27-FEB-2003.
XX
PF 14-AUG-2002; 2002WO-US025765.
XX
PR 14-AUG-2001; 2001US-0312147P.
PR 01-NOV-2001; 2001US-0346382P.
PR 26-NOV-2001; 2001US-0333347P.
XX
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
XX
PI Woolf C, D'urso D, Befort K, Costigan M;
XX
DR WPI; 2003-268312/26.
DR GENBANK; L22655.
XX
PT New composition comprising two or more isolated polypeptides, useful for
PT preparing a medicament for treating pain in an animal.
XX
PS Claim 1; Page; 1017pp; English.
XX
CC The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a rat protein (shown in Table 2 of
CC the specification) which is differentially expressed during pain. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 239 AA;

Query Match 85.1%; Score 589; DB 7; Length 239;
Best Local Similarity 84.7%; Pred. No. 2e-45;
Matches 111; Conservative 13; Mismatches 7; Indels 0; Gaps 0;

Qy 2 MSPAQFLFLLVLWIRETNGYVVMTQTPLTLSVTIGQPASISCKSSQSLLSDGKTYLNWL 61

Db |||||||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
1 MSPAQFLFLLMLWIQETSGDVVMTQTPVSLSVAIGQPASISCKSSQSLVGTNGKTYLNWL 60

Qy 62 LQRPGQSPKRЛИYLVSKLDGVPDRFTGSGSGTDFTLKISRIEAEDLGLYYCWQGTHFPR 121
|||:|||:|||:|||:
Db 61 LQRPGQSPKRЛИYLVSKLDGIPDRFSGSGSETDFTLKISRVEADDLGVYYCLQGTHFPL 120

Qy 122 TFGGGTKLEIK 132
|||:|||:
Db 121 TFGSGTKLEIK 131

RESULT 13

AAE03751

ID AAE03751 standard; protein; 113 AA.

XX

AC AAE03751;

XX

DT 07-AUG-2001 (first entry)

XX

DE Murine PSCA Ab light chain variable region domain from clone 6B8.1D7.2B3.

XX

KW Murine; prostate stem cell antigen; PSCA; cytostatic; gene therapy;

KW glycoprotein; cancer; prostate; bladder; lung; tumour; Ab; antibody;

KW light chain variable domain; VL.

XX

OS Mus musculus.

XX

FH Key Location/Qualifiers

FT Region 24. .39

FT /label= CDR1

FT /note= "Complementarity determining region 1"

FT Region 55. .61

FT /label= CDR2

FT /note= "Complementarity determining region 2"

FT Region 94. .102

FT /label= CDR3

FT /note= "Complementarity determining region 3"

XX

PN WO200140309-A2.

XX

PD 07-JUN-2001.

XX

PF 27-OCT-2000; 2000WO-US029603.

XX

PR 29-OCT-1999; 99US-0162558P.

PR 16-FEB-2000; 2000US-0182872P.

XX

PA (GETH) GENENTECH INC.

XX

PI Devaux B, Keller G, Koeppen H, Lasky LA;

XX

DR WPI; 2001-389954/41.

XX

PT Novel anti-prostate stem cell antigen (PSCA) antibody that internalizes

PT on binding to PSCA on mammalian cell and inhibits growth of PSCA-

PT expressing cancer cells in vivo, useful for killing PSCA-expressing

PT cancer cells.
XX
PS Claim 22; Fig 12; 112pp; English.
XX
CC The present sequence is murine prostate stem cell antigen (PSCA) antibody
CC (Ab) light chain variable region domain (VL) from hybridoma clone
CC 6B8.1D7.2B3, Asc# 2761. PSCA is a single subunit glycoprotein that is
CC expressed on the cell surface as a glycosylphosphatidylinositol (GPI)-
CC anchored protein. The present invention relates to anti-PSCA antibody
CC composition and methods of killing PSCA-expressing cancer cells. PSCA is
CC useful for inhibiting and killing the growth of PSCA-expressing cancer
CC cells such as prostate cancer, bladder cancer or lung cancer cells.
CC Humanised antibody conjugated to a toxin or a radioactive isotope is used
CC for killing the cancer cells. PSCA is useful for specifically targetting
CC PSCA-expressing tumour cells in vivo and for inhibiting or killing these
CC cells. The antibodies are also useful for treating the above mentioned
CC cancers and for diagnosing and staging of PSCA-expressing cancer, for
CC purification or immunoprecipitation of PSCA from cells, and for detection
CC and quantitation of PSCA in vitro. PSCA DNA is also useful for treating
CC cancers by gene therapy techniques
XX
SQ Sequence 113 AA;

Query Match 82.5%; Score 571; DB 4; Length 113;
Best Local Similarity 97.3%; Pred. No. 3.7e-44;
Matches 108; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 22 VVMTQTPLTLSVTIGQPASISCKSSQSLLSDGKTYLNWLLQRPGQSPKRLIYLVSKLDS 81
Db 2 VVMTQTPLTLSVTIGQPASISCKSSQSLLSDGKTYLNWLLQRPGQSPKRLIYLVSTLDS 61

Qy 82 GVPDRFTGSGSGTDFTLKISRVEAEDLGLYYCWQGTHFPRTFGGGTKLEIK 132
Db 62 GVPDRFTGSGSGTDFTLKISRVEAEDLGVYYCWQGTHFPRTFGGGTKLEIK 112

RESULT 14
AAE03756
ID AAE03756 standard; protein; 218 AA.
XX
AC AAE03756;
XX
DT 11-SEP-2003 (revised)
DT 07-AUG-2001 (first entry)
XX
DE Chimeric antibody 6B8 Fab light chain (6B8.1D7.2B3).
XX
KW Murine; prostate stem cell antigen; PSCA; cytostatic; gene therapy;
KW glycoprotein; cancer; prostate; bladder; lung; tumour; Ab; antibody;
KW human; antibody binding fragment; Fab; light chain region.
XX
OS Mus musculus.
OS Homo sapiens.
OS Chimeric.
XX
FH Key Location/Qualifiers
FT Region 1. .113

FT /note= "Derived from mouse light chain variable region
FT (VL)"
FT Region 114. .218
FT /note= "Derived from human kappa light chain constant
FT region (Ckappa)"
XX
PN WO200140309-A2.
XX
PD 07-JUN-2001.
XX
PF 27-OCT-2000; 2000WO-US029603.
XX
PR 29-OCT-1999; 99US-0162558P.
PR 16-FEB-2000; 2000US-0182872P.
XX
PA (GETH) GENENTECH INC.
XX
PI Devaux B, Keller G, Koeppen H, Lasky LA;
XX
DR WPI; 2001-389954/41.
XX
PT Novel anti-prostate stem cell antigen (PSCA) antibody that internalizes
PT on binding to PSCA on mammalian cell and inhibits growth of PSCA-
PT expressing cancer cells in vivo, useful for killing PSCA-expressing
PT cancer cells.
XX
PS Claim 5; Fig 13; 112pp; English.
XX
CC The present chimeric sequence is full length 2761 antibody binding
CC fragment (Fab) light chain (6B8.1D7.2B3) derived from murine light chain
CC variable region (VL) and human kappa light chain constant region. This
CC antibody binds to prostate stem cell antigen (PSCA) which is a single
CC subunit glycoprotein that is expressed on the cell surface as a
CC glycosylphosphatidylinositol (GPI)-anchored protein. The present
CC invention relates to anti-PSCA antibody composition and methods of
CC killing PSCA-expressing cancer cells. PSCA is useful for inhibiting and
CC killing the growth of PSCA-expressing cancer cells such as prostate
CC cancer, bladder cancer or lung cancer cells. Humanised antibody
CC conjugated to a toxin or a radioactive isotope is used for killing the
CC cancer cells. PSCA is useful for specifically targetting PSCA-expressing
CC tumour cells in vivo and for inhibiting or killing these cells. The
CC antibodies are also useful for treating the above mentioned cancers and
CC for diagnosing and staging of PSCA-expressing cancer, for purification or
CC immunoprecipitation of PSCA from cells, and for detection and
CC quantitation of PSCA in vitro. PSCA DNA is also useful for treating
CC cancers by gene therapy techniques. (Updated on 11-SEP-2003 to
CC standardise OS field)
XX
SQ Sequence 218 AA;

Query Match 82.5%; Score 571; DB 4; Length 218;
Best Local Similarity 97.3%; Pred. No. 7.8e-44;
Matches 108; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 22 VVMTQTPLTLSVTIGQPASISCKSSQSLLSDGKTYLNWLLQRPGQSPKRLIYLVSKLDS 81
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2 VVMTQTPLTLSVTIGQPASISCKSSQSLLSDGKTYLNWLLQRPGQSPKRLIYLVSTLDS 61

Qy 82 GVPDRFTGSGSGTDFTLKISR~~E~~AEDLGLYYCWQGTHF~~P~~RTFGGGTKLEIK 132
||| :||||| :||||| :||||| :||||| :||||| :||||| :|||
Db 62 GVPDRFTGSGSGTDFTLKISR~~V~~EAEDLGVYYCWQGTHF~~P~~RTFGGGTKLEIK 112

RESULT 15
AAY06273
ID AAY06273 standard; protein; 353 AA.
XX
AC AAY06273;
XX
DT 23-AUG-1999 (first entry)
XX
DE Anti Fc alpha receptor scFv A77-PDGR-R TM fusion.
XX
KW Single chain antibody; scFv; A77; IgA receptor; Fc receptor;
KW Fc alpha receptor; platelet derived growth factor receptor;
KW antibody engineering; cell surface expression; therapy; cancer; tumour;
KW vaccine; human.
XX
OS Mus sp.
OS Synthetic.
OS Chimeric.
XX
FH Key Location/Qualifiers
FT Domain 1. .21
FT /note= "Ig K-chain SP"
FT Peptide 22. .30
FT /note= "HA epitope"
FT Domain 38. .160
FT /note= "A77 VL"
FT Peptide 161. .175
FT /note= "linker"
FT Domain 176. .287
FT /note= "A77 VH"
FT Peptide 294. .303
FT /note= "Myc epitope"
FT Domain 304. .353
FT /note= "PDGFR transmembrane domain"
XX
PN WO9928349-A2.
XX
PD 10-JUN-1999.
XX
PF 02-DEC-1998; 98WO-US025556.
XX
PR 02-DEC-1997; 97US-0067232P.
XX
PA (MEDA-) MEDAREX INC.
XX
PI Keler T, Goldstein J, Graziano R, Deo YM;
XX
DR WPI; 1999-371099/31.
DR N-PSDB; AAX58936.
XX
PT Cells expressing anti-Fc receptor binding components.

XX

PS Example 6; Fig 10A-E; 68pp; English.

XX

CC The present sequence represents a fusion protein comprising murine anti-
CC Fc alpha receptor antibody A77 sFv and the transmembrane domain of
CC platelet derived growth factor receptor (PDFR-R TM). It is encoded by
CC expression vector pJG718 (see AAX58935). Murine tumour cells transformed
CC to express A77-TM were able to bind a soluble form of the Fc alpha
CC receptor, and the bound receptor was able to engage IgA molecules. This
CC is an example of cells of the invention that have been transformed to
CC express on their surface a component which binds to an Fc receptor of an
CC effector cell. The transformed cell is targeted to an effector cell via
CC the Fc binding component, and can be used as a vehicle to increase an
CC effector cell-mediated immune response, such as cell lysis and
CC phagocytosis, against an antigen associated with the cell. The
CC transformed cells are used to treat cancer and infectious diseases or
CC used as vaccines. The method allows for killing of target cells without
CC targeting any particular antigen on the cell. This is advantageous since
CC many tumour cells and other target cells do not have defined antigens for
CC targeting

XX

SQ Sequence 353 AA;

Query Match 81.2%; Score 562; DB 2; Length 353;
Best Local Similarity 94.6%; Pred. No. 8.7e-43;
Matches 105; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 22 VVMTQTPLTLSVTIGQPASISCKSSQSLLSDGKTYLNWLLQRPGQSPKRLIYLVSKLDS 81
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Db 177 VVMTQTPLTLSITIGQPASISCKSSQSLLSDGKTYLNWLLQRPGQSPTRLIYLVSKLDS 236

Qy 82 GVPDRFTGSGSGTDFTLKISRVEAEDLGLYYCWQGTHFPRTFGGGTKLEIK 132
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Db 237 GVPDRFTGSGSGTDFTLKISRVEAEDLGIVYCWQGAHFPQTFGGGTKLEIK 287

Search completed: May 17, 2004, 11:30:33

Job time : 52.3556 secs

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OM protein - protein search, using sw model

Run on: May 17, 2004, 11:29:03 ; Search time 16.1333 Seconds
(without alignments)
422.394 Million cell updates/sec

Title: US-10-010-942B-2
Perfect score: 692
Sequence: 1 MMSPAQFLFLVLWIRETNG.....CWQGTHFPRTFGGGTKLEIK 132

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:
*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query			Description	
		Match	Length	DB	ID	
1	649	93.8	131	4	US-09-647-468-163	Sequence 163, App
2	646	93.4	131	4	US-09-647-468-164	Sequence 164, App
3	562	81.2	353	4	US-09-203-958A-4	Sequence 4, Appli
4	560	80.9	112	4	US-09-809-739-11	Sequence 11, Appli
5	559	80.8	112	4	US-09-647-468-149	Sequence 149, App
6	559	80.8	112	4	US-09-647-468-150	Sequence 150, App
7	548	79.2	112	2	US-08-678-194-6	Sequence 6, Appli
8	548	79.2	112	3	US-08-890-011-6	Sequence 6, Appli
9	548	79.2	112	4	US-09-262-724-6	Sequence 6, Appli
10	548	79.2	535	4	US-08-983-035A-38	Sequence 38, Appli
11	538	77.7	112	4	US-09-809-739-16	Sequence 16, Appli

12	537	77.6	132	1	US-08-477-877B-91	Sequence 91, Appl
13	537	77.6	132	2	US-08-472-281A-91	Sequence 91, Appl
14	537	77.6	132	2	US-08-477-989B-91	Sequence 91, Appl
15	533	77.0	112	4	US-09-809-739-17	Sequence 17, Appl
16	530	76.6	112	4	US-09-809-739-15	Sequence 15, Appl
17	525	75.9	112	4	US-09-809-739-18	Sequence 18, Appl
18	520	75.1	112	4	US-09-809-739-14	Sequence 14, Appl
19	518	74.9	132	1	US-08-477-877B-84	Sequence 84, Appl
20	518	74.9	132	2	US-08-472-281A-84	Sequence 84, Appl
21	518	74.9	132	2	US-08-477-989B-84	Sequence 84, Appl
22	515	74.4	135	1	US-08-259-372A-12	Sequence 12, Appl
23	515	74.4	135	1	US-08-468-671-12	Sequence 12, Appl
24	512	74.0	112	3	US-09-184-658-49	Sequence 49, Appl
25	512	74.0	112	4	US-09-504-262D-49	Sequence 49, Appl
26	508	73.4	289	3	US-09-184-658-63	Sequence 63, Appl
27	508	73.4	289	4	US-09-504-262D-63	Sequence 63, Appl
28	504	72.8	113	3	US-09-214-095D-116	Sequence 116, App
29	504	72.8	242	4	US-09-479-614-20	Sequence 20, Appl
30	493.5	71.3	114	2	US-08-672-345C-9	Sequence 9, Appli
31	493.5	71.3	114	3	US-09-214-095D-9	Sequence 9, Appli
32	485	70.1	115	2	US-08-672-345C-99	Sequence 99, Appl
33	468	67.6	112	1	US-08-477-877B-89	Sequence 89, Appl
34	468	67.6	112	2	US-08-472-281A-89	Sequence 89, Appl
35	468	67.6	112	2	US-08-477-989B-89	Sequence 89, Appl
36	466	67.3	111	4	US-09-809-739-13	Sequence 13, Appl
37	465	67.2	112	1	US-08-477-877B-88	Sequence 88, Appl
38	465	67.2	112	2	US-08-472-281A-88	Sequence 88, Appl
39	465	67.2	112	2	US-08-477-989B-88	Sequence 88, Appl
40	463	66.9	131	1	US-08-129-930B-95	Sequence 95, Appl
41	463	66.9	131	3	US-08-134-346A-50	Sequence 50, Appl
42	463	66.9	131	4	US-08-976-288A-95	Sequence 95, Appl
43	461	66.6	112	1	US-07-942-245-28	Sequence 28, Appl
44	458	66.2	149	4	US-09-192-838B-2	Sequence 2, Appli
45	458	66.2	149	4	US-09-324-191-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1

US-09-647-468-163

```
; Sequence 163, Application US/09647468
; Patent No. 6677436
; GENERAL INFORMATION:
; APPLICANT: SATO, KOH
; APPLICANT: ADACHI, HIDEKI
; APPLICANT: YABUTA, NAOHIRO
; TITLE OF INVENTION: HUMANIZED ANTIBODY AGAINST HUMAN TISSUE FACTOR (TF) AND
; TITLE OF INVENTION: PROCESS OF PRODUCTION OF THE HUMANIZED ANTIBODY
; FILE REFERENCE: 053466/0289
; CURRENT APPLICATION NUMBER: US/09/647,468
; CURRENT FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: PCT/JP99/01768
; PRIOR FILING DATE: 1999-04-02
; PRIOR APPLICATION NUMBER: JP 10-91850
; PRIOR FILING DATE: 1998-04-03
; NUMBER OF SEQ ID NOS: 183
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; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 163
; LENGTH: 131
; TYPE: PRT
; ORGANISM: Mus sp.
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Amino acid
; OTHER INFORMATION: sequence coding for L chain V region of ant-TF
; OTHER INFORMATION: mouse monoclonal antibody ATR-7
US-09-647-468-163

Query Match 93.8%; Score 649; DB 4; Length 131;
Best Local Similarity 93.9%; Pred. No. 4.1e-55;
Matches 123; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 2 MSPAQFLFLLVLWIRETNGYVVMQTPLTLSVTIGQPASISCKSSQSLLSDGKTYLNWL 61
|||:|||||:||||| ||| |||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 MSPAQFLFLLVLWIREINGDVVLTQTPLTLSVTIGQPASVSCKSSQSLLSDGKTYLNWL 60

Qy 62 LQRPGQSPKRЛИYLVSKLDGVPDRFTGSGSGTDFTLKISRVEAEDLGLYYCWQGTHFPR 121
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 LQRPGQSPKRЛИYLVSKLDGVPDRFTGSGSGTDFTLKISRVEAEDLGVYYCWQDTHFPD 120

Qy 122 TFGGGTKLEIK 132
|||||:|||||
Db 121 TFGGGTKLEIK 131

RESULT 2

US-09-647-468-164

; Sequence 164, Application US/09647468
; Patent No. 6677436
; GENERAL INFORMATION:
; APPLICANT: SATO, KOH
; APPLICANT: ADACHI, HIDEKI
; APPLICANT: YABUTA, NAOHIRO
; TITLE OF INVENTION: HUMANIZED ANTIBODY AGAINST HUMAN TISSUE FACTOR (TF) AND
; TITLE OF INVENTION: PROCESS OF PRODUCTION OF THE HUMANIZED ANTIBODY
; FILE REFERENCE: 053466/0289
; CURRENT APPLICATION NUMBER: US/09/647,468
; CURRENT FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: PCT/JP99/01768
; PRIOR FILING DATE: 1999-04-02
; PRIOR APPLICATION NUMBER: JP 10-91850
; PRIOR FILING DATE: 1998-04-03
; NUMBER OF SEQ ID NOS: 183
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 164
; LENGTH: 131
; TYPE: PRT
; ORGANISM: Mus sp.
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Amoino acid
; OTHER INFORMATION: sequence coding for L chain V region of ant-TF
; OTHER INFORMATION: mouse monoclonal antibody ATR-8
US-09-647-468-164

Query Match 93.4%; Score 646; DB 4; Length 131;
 Best Local Similarity 93.1%; Pred. No. 7.9e-55;
 Matches 122; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

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Qy      2 MSPAQFLFLLVLWIRETNGYVVMQTPLTLSVTIGQPASISCKSSQSLLSDGKTYLNWL 61
        |||||||:|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||
Db      1 MSPAQFLFLLVLWIRDINGDVVLQTPLTLSVTIGQPASVSCCKSSQSLLSDGKTYLNWL 60

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```

Qy      62 LQRPGQSPKRЛИYLVSKLDGVPDRFTGSGSGTDFTLKISRVEAEDLGLYYCWQGTHFPR 121
        |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||
Db      61 LQRPGQSPKRЛИYLVSKLDGVPDRFTGSGSGTDFTLKISRVEAEDLGVYYCWQDTHFPD 120

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Qy      122 TFGGGTKLEIK 132
        |||||||:|||
Db      121 TFGGGTKLEIK 131

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RESULT 3

US-09-203-958A-4

; Sequence 4, Application US/09203958A
 ; Patent No. 6682928
 ; GENERAL INFORMATION:
 ; APPLICANT: KELER, Tibor
 ; APPLICANT: GOLDSTEIN, Joel
 ; APPLICANT: GRAZIANO, Robert
 ; APPLICANT: DEO, Yashwant M.
 ; TITLE OF INVENTION: CELLS EXPRESSING ANTI-FC RECEPTOR
 ; TITLE OF INVENTION: BINDING COMPONENTS
 ; FILE REFERENCE: MXI-099CPA
 ; CURRENT APPLICATION NUMBER: US/09/203,958A
 ; CURRENT FILING DATE: 1998-12-02
 ; PRIOR APPLICATION NUMBER: 60/067232
 ; PRIOR FILING DATE: 1997-12-02
 ; NUMBER OF SEQ ID NOS: 4
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 4
 ; LENGTH: 353
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Synthetic construct

US-09-203-958A-4

Query Match 81.2%; Score 562; DB 4; Length 353;
 Best Local Similarity 94.6%; Pred. No. 2.8e-46;
 Matches 105; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

```

Qy      22 VVMTQTPLTLSVTIGQPASISCKSSQSLLSDGKTYLNWLQRPQSPKRЛИYLVSKLDS 81
        |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||
Db      177 VVMTQTPLTLSITIGQPASISCKSSQSLLSDGKTYLNWLQRPQSPTRЛИYLVSKLDS 236

```

```

Qy      82 GVPDRFTGSGSGTDFTLKISRVEAEDLGLYYCWQGTHFPRTFGGGTKEIK 132
        |||||||:|||||:|||||:|||||:|||||:|||||:|||:|||||:|||
Db      237 GVPDRFTGSGSGTDFTLKISRVEAEDLGИYYCWQGAHFPQTFGGGTKLEIK 287

```

RESULT 4

US-09-809-739-11
; Sequence 11, Application US/09809739
; Patent No. 6663863
; GENERAL INFORMATION:
; APPLICANT: Horvath, Christopher J.
; APPLICANT: Rao, Patricia E.
; TITLE OF INVENTION: Method of Inhibiting Stenosis and
; TITLE OF INVENTION: Restenosis
; FILE REFERENCE: 1855.1069-003
; CURRENT APPLICATION NUMBER: US/09/809,739
; CURRENT FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: US 09/528,267
; PRIOR FILING DATE: 2000-03-17
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1)...(112)
; OTHER INFORMATION: Murine mAb 1D9 light chain variable region
; NAME/KEY: SITE
; LOCATION: (24)...(39)
; OTHER INFORMATION: CDR1
; NAME/KEY: SITE
; LOCATION: (55)...(61)
; OTHER INFORMATION: CDR2
; NAME/KEY: SITE
; LOCATION: (94)...(102)
; OTHER INFORMATION: CDR3
; OTHER INFORMATION: Mouse
US-09-809-739-11

Query Match 80.9%; Score 560; DB 4; Length 112;
Best Local Similarity 94.6%; Pred. No. 1.2e-46;
Matches 105; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 22 VVMTQTPLTLSVTIGQPASISCKSSQSLLSDGKTYLNWLLQRPGQSPKRLIYLVSK LDS 81
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 2 VVMTQTPLTLSVTVGHPASISCKSSQSLLSDGKTFLNWLLQRPGQSPKRLIYLVSK LDS 61

Qy 82 GVPDRFTGSGSGTDFTLKISRVEAEDLGYYCWQGTHFPRTFGGGTKLEIK 132
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 62 GVPDRFTGSGSGTDFTLKISRVEAEDLGYYCWQGTHFPYTFGGGTKEIK 112

RESULT 5
US-09-647-468-149
; Sequence 149, Application US/09647468
; Patent No. 6677436
; GENERAL INFORMATION:
; APPLICANT: SATO, KOH
; APPLICANT: ADACHI, HIDEKI
; APPLICANT: YABUTA, NAOHIRO
; TITLE OF INVENTION: HUMANIZED ANTIBODY AGAINST HUMAN TISSUE FACTOR (TF) AND

; TITLE OF INVENTION: PROCESS OF PRODUCTION OF THE HUMANIZED ANTIBODY
; FILE REFERENCE: 053466/0289
; CURRENT APPLICATION NUMBER: US/09/647,468
; CURRENT FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: PCT/JP99/01768
; PRIOR FILING DATE: 1999-04-02
; PRIOR APPLICATION NUMBER: JP 10-91850
; PRIOR FILING DATE: 1998-04-03
; NUMBER OF SEQ ID NOS: 183
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 149
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Mus sp.
; FEATURE:
; OTHER INFORMATION: Amino acid sequence of L chain V region of anti-TF mouse
; OTHER INFORMATION: monoclonal antibody ATR-7
US-09-647-468-149

Query Match 80.8%; Score 559; DB 4; Length 112;
Best Local Similarity 94.6%; Pred. No. 1.5e-46;
Matches 105; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy	22	VVMTQTPLTLSVTIGQPASISCKSSQSLLSDGKTYLNWLLQRPGQSPKRLIYLVSKLDS	81
	: : : : : : : : : : : :		
Db	2	VVLTQTPLTLSVTIGQPASVSCKSSQSLLSDGKTYLNWLLQRPGQSPKRLIYLVSKLDS	61
Qy	82	GVPDRFTGSGSGTDFTLKISRVEAEDLGLYYCWQGTHFPRTFGGGTKLEIK	132
	: : : : : : : : : : :		
Db	62	GVPDRFTGSGSGTDFTLKISRVEAEDLGVYYCWQDTHFPDTFGGGTKLEIK	112

RESULT 6

US-09-647-468-150
; Sequence 150, Application US/09647468
; Patent No. 6677436
; GENERAL INFORMATION:
; APPLICANT: SATO, KOH
; APPLICANT: ADACHI, HIDEKI
; APPLICANT: YABUTA, NAOHIRO
; TITLE OF INVENTION: HUMANIZED ANTIBODY AGAINST HUMAN TISSUE FACTOR (TF) AND
; TITLE OF INVENTION: PROCESS OF PRODUCTION OF THE HUMANIZED ANTIBODY
; FILE REFERENCE: 053466/0289
; CURRENT APPLICATION NUMBER: US/09/647,468
; CURRENT FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: PCT/JP99/01768
; PRIOR FILING DATE: 1999-04-02
; PRIOR APPLICATION NUMBER: JP 10-91850
; PRIOR FILING DATE: 1998-04-03
; NUMBER OF SEQ ID NOS: 183
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 150
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Mus sp.
; FEATURE:
; OTHER INFORMATION: Amino acid sequence of L chain V region of anti-TF mouse

; OTHER INFORMATION: monoclonal antibody ATR-8
US-09-647-468-150

Query Match 80.8%; Score 559; DB 4; Length 112;
Best Local Similarity 94.6%; Pred. No. 1.5e-46;
Matches 105; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 22 VVMTQTPLTLSVTIGQPASISCKSSQSLLSDGKTYLNWLLQRPGQSPKRLIYLVSKLDS 81
||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 2 VVLTQTPLTLSVTIGQPASVCKSSQSLLSDGKTYLNWLLQRPGQSPKRLIYLVSKLDS 61

QY 82 GVPDRFTGSGSGTDFTLKISRVEAEDLGLYYCWQGTHFPRTFGGGTKLEIK 132
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 62 GVPDRFTGSGSGTDFTLKISRVEAEDLGVYYCWQDTHFPDTFGGGTKLEIK 112

RESULT 7

US-08-678-194-6

; Sequence 6, Application US/08678194
; Patent No. 5922845
; GENERAL INFORMATION:
; APPLICANT: Deo, Yashwant M.
; APPLICANT: Graziano, Robert
; APPLICANT: Keler, Tibor
; TITLE OF INVENTION: Therapeutic Multispecific Compounds
; TITLE OF INVENTION: Comprised of Anti-Fc{SYMBOL 97 \f "Symbol"} Receptor Antibodi
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, Suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/678,194
; FILING DATE: July 11, 1996
; PRIOR APPLICATION DATA: No. 5922845e
; APPLICATION NUMBER: US
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Beth A. Arnold
; REGISTRATION NUMBER: 35,430
; REFERENCE/DOCKET NUMBER: MXI-064
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 112 amino acids
; TYPE: amino acid

; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-890-011-6

Query Match 79.2%; Score 548; DB 3; Length 112;
Best Local Similarity 91.0%; Pred. No. 1.7e-45;
Matches 101; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

Qy 22 VVMTQTPLTLSVTIGQPASISCKSSQSLLSDGKTYLNWLLQRPGQSPKRЛИYLVSKLDS 81
: :||:||||:|||||||||||||||||||||||||||||||||
Db 2 IQLTQSPLTLSITIGQPASISCKSSQSLLSDGKTYLNWLLQRPGQSPTRЛИYLVSKLDS 61
Qy 82 GVPDRFTGSGSGTDFTLKISRVEAEDLGLYYCWQGTHFPRTFGGGTKLEIK 132
|||||||||||||||||:|||||:||||| |||:|||||||||
Db 62 GVPDRFTGSGSGTDFTLKISRVEAEDLGIYYCWQGAHFQTFGGGTKEIK 112

RESULT 9

US-09-262-724-6

; Sequence 6, Application US/09262724
; Patent No. 6303755
; GENERAL INFORMATION:
; APPLICANT: Deo, Yashwant M.
; Graziano, Robert
; Keler, Tibor
; TITLE OF INVENTION: Therapeutic Multispecific Compounds
; Comprised of Anti-Fc{SYMBOL 97 \f "Symbol"}
; Receptor Antibodies
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, Suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/262,724
; FILING DATE: 04-Mar-1999
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/678,194
; FILING DATE: July 11, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Beth A. Arnold
; REGISTRATION NUMBER: 35,430
; REFERENCE/DOCKET NUMBER: MXI-064
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:

; LENGTH: 112 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-262-724-6

Query Match 79.2%; Score 548; DB 4; Length 112;
Best Local Similarity 91.0%; Pred. No. 1.7e-45;
Matches 101; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

Qy 22 VVMTQTPLTLSVTIGQPASISCKSSQSLLSDGKTYLNWLLQRPGQSPKRLIYLVSKLD 81
: :||:||||:|||||||||||||||||||||||||||||||||
Db 2 IQLTQSPLTLSITIGQPASISCKSSQSLLSDGKTYLNWLLQRPGQSPTRLIYLVSKLD 61

Qy 82 GVPDRFTGSGSGTDFTLKISRVEAEDLGLYYCWQGTHFPRTFGGGTKLEIK 132
||||||||||||||||:|||||:||||| |||:|||||||||
Db 62 GVPDRFTGSGSGTDFTLKISRVEAEDLGIYYCWQGAHFQTFGGGTKEIK 112

RESULT 10
US-08-983-035A-38
; Sequence 38, Application US/08983035A
; Patent No. 6326464
; GENERAL INFORMATION:
; APPLICANT: CONSEILLER, EMMANUEL
; BRACCO, LAURENT
; TITLE OF INVENTION: P53 PROTEIN VARIANTS AND THERAPEUTICAL
; USES THEREOF
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FINNEGAN, HENDERSON, FARABOW, GARRETT &
; DUNNER, LLP
; STREET: 1300 I Street, NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/983,035A
; FILING DATE: 20-Feb-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/FR96/01111
; FILING DATE: 17-JUL-1996
; APPLICATION NUMBER: FR 95/08729
; FILING DATE: 19-JUL-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Strauss, William L.
; REGISTRATION NUMBER: 47,114
; REFERENCE/DOCKET NUMBER: 03804.0142
; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 202-408-4000
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 535 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 38:
US-08-983-035A-38

Query Match 79.2%; Score 548; DB 4; Length 535;
Best Local Similarity 92.8%; Pred. No. 1e-44;
Matches 103; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Qy 22 VVMTQTPLTLSVTIGQPASISCKSSQSLLSDGKTYLNWLLQRPGQSPKRLIYLVSKLDS 81
|:|||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 135 VLMTQTPLTLSVTIGQPASISCKSSQSLLSDGKTYLNWLLQRPGQSPKRLIYLVSKLDS 194

Qy 82 GVPDRFTGSGSGTDFTLKISREREAEDLGLYYCWQGTHFPRTFGGGTKLEIK 132
|||||||||||||||||:|:||||||:||||||| | ||| |||||:|
Db 195 GVPDRFTGSGSGTDFTLKINRVEAEDLGVYYCWQGTHSPLTFGAGTKLELK 245

RESULT 11

US-09-809-739-16

; Sequence 16, Application US/09809739
; Patent No. 6663863
; GENERAL INFORMATION:
; APPLICANT: Horvath, Christopher J.
; APPLICANT: Rao, Patricia E.
; TITLE OF INVENTION: Method of Inhibiting Stenosis and
; TITLE OF INVENTION: Restenosis
; FILE REFERENCE: 1855.1069-003
; CURRENT APPLICATION NUMBER: US/09/809,739
; CURRENT FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: US 09/528,267
; PRIOR FILING DATE: 2000-03-17
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized sequence
US-09-809-739-16

Query Match 77.7%; Score 538; DB 4; Length 112;
Best Local Similarity 89.2%; Pred. No. 1.5e-44;
Matches 99; Conservative 10; Mismatches 2; Indels 0; Gaps 0;

Qy 22 VVMTQTPLTLSVTIGQPASISCKSSQSLLSDGKTYLNWLLQRPGQSPKRLIYLVSKLDS 81
|||||:||:| ||:||||||| |||||||:|||||:|||||:|||||:|||
Db 2 VVMTQSPLSLPVTLGQPASISCKSSQSLLSDGKTFLNWLLQRPGQSPRRLIYLVSKLDS 61

Qy 82 GVPDRFTGSGSGTDFTLKISREREAEDLGLYYCWQGTHFPRTFGGGTKLEIK 132

|||||:|||||:|||||:||||:||:|||||:|||:|||:|||:|||:|||:
Db 62 GVPDRFSGSGSGTDFTLKISRVEAEDVGYYCWQGTHFPYTFGGGTRLEIK 112

RESULT 12
US-08-477-877B-91
; Sequence 91, Application US/08477877B
; Patent No. 5730979
; GENERAL INFORMATION:
; APPLICANT: Bazin, Herv
; APPLICANT: Latinne, Dominique
; TITLE OF INVENTION: LO-CD2a Antibody and Uses Thereof for Inhibiting T-
Cell Activati
; NUMBER OF SEQUENCES: 96
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carella, Byrne, Bain, Gilfillan,
; ADDRESSEE: Cecchi, Stewart & Olstein
; STREET: 6 Becker Farm Road
; CITY: Roseland
; STATE: New Jersey
; COUNTRY: U.S.A.
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch diskette
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,877B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/407,009
; FILING DATE: 29-MAR-1995
; APPLICATION NUMBER: 08/119,032
; FILING DATE: 09-SEP-1993
; APPLICATION NUMBER: 08/027,008
; FILING DATE: 05-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Olstein, Elliot M.
; REGISTRATION NUMBER: 24,025
; REFERENCE/DOCKET NUMBER: 61750-146
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 91:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 132 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: polypeptide
; FEATURE:
; NAME/KEY: Humanized LO-CD2a light chain variable region.
US-08-477-877B-91

Query Match 77.6%; Score 537; DB 1; Length 132;

Best Local Similarity 78.8%; Pred. No. 2.3e-44;
Matches 104; Conservative 12; Mismatches 16; Indels 0; Gaps 0;

Qy 1 MMSPAQFLFLLVLWIRETNGYVVMTQTPLTLSVTIGQPASISCKSSQSLLSDGKTYLNW 60
||||| | ||||:||| ||| |||||:| :| ||:|||||||:||||| | | |||||
Db 1 MMSPVQSLFLLLWLGTNGDVVMTQSPPSLLVTLGQPASISCRSSQSLLHSSGNTYLNW 60

Qy 61 LLQRPGQSPKRLIYLVSKLDGVPDRFTGSGSGTDFTLKISRERIEAEDLGLYYCWQGTHFP 120
|||||||: |||||||:|||||:|||||:|||||:|||||:|:||| | ||:|
Db 61 LLQRPGQSPQPLIYLVSKLESGVPDFRGSGSGTDFTLKISGVREAEDVGVYYCMQFTHYP 120

Qy 121 RTFGGGTKLEIK 132
||| |||||||
Db 121 YTFGQGTKLEIK 132

RESULT 13

US-08-472-281A-91

; Sequence 91, Application US/08472281A
; Patent No. 5817311
; GENERAL INFORMATION:
; APPLICANT: Bazin, Herv
; APPLICANT: Latinne, Dominique
; TITLE OF INVENTION: LO-CD2a Antibody and Uses Thereof for Inhibiting T-
Cell Activati
; NUMBER OF SEQUENCES: 96
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carella, Byrne, Bain, Gilfillan,
; ADDRESSEE: Cecchi, Stewart & Olstein
; STREET: 6 Becker Farm Road
; CITY: Roseland
; STATE: New Jersey
; COUNTRY: U.S.A.
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch diskette
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/472,281A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/407,009
; FILING DATE: 29-MAR-1995
; APPLICATION NUMBER: 08/119,032
; FILING DATE: 09-SEP-1993
; APPLICATION NUMBER: 08/027,008
; FILING DATE: 05-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Olstein, Elliot M.
; REGISTRATION NUMBER: 24,025
; REFERENCE/DOCKET NUMBER: 61750-142
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744

; INFORMATION FOR SEQ ID NO: 91:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 132 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: polypeptide
; FEATURE:
; NAME/KEY: Humanized LO-CD2a light chain variable region.
US-08-472-281A-91

Query Match 77.6%; Score 537; DB 2; Length 132;
Best Local Similarity 78.8%; Pred. No. 2.3e-44;
Matches 104; Conservative 12; Mismatches 16; Indels 0; Gaps 0;

Qy 1 MMSPAQFLFLLVLWIRETNGYVVMQTPLTLSVTIGQPASISCKSSQSLLSDGKTYLNW 60
||| || | ||||:||| ||| |||||:| :| ||:|||||||:|||||| | | |||||
Db 1 MMSPVQSLFLLLWILGTNGDVVMTQSPPSLLVTLGQPASISCRSSQSLLHSSGNTYLNW 60

Qy 61 LLQRPGQSPKRЛИYLVSKLDGVPDRFTGSGSGTDFTLKISRIEAEDLGLYYCWQGTHFP 120
|||||: ||||||:|||||:|||||:|||||:|||||:|||||:|:||| | ||:|
Db 61 LLQRPGQSPQPLIYLVSKLESGVPDFSGSGSGTDFTLKISGVEAEDVGVYYCMQFTHYP 120

Qy 121 RTFGGGTKLEIK 132
||| |||||||
Db 121 YTFGQGTKLEIK 132

RESULT 14
US-08-477-989B-91
; Sequence 91, Application US/08477989B
; Patent No. 5951983
; GENERAL INFORMATION:
; APPLICANT: Bazin, Herv
; APPLICANT: Latinne, Dominique
; APPLICANT: Kaplan, Ruth
; APPLICANT: Kieber-Emmons, Thomas
; APPLICANT: Postema, Christina E.
; APPLICANT: White-Scharf, Mary
; TITLE OF INVENTION: LO-CD2a Antibody and Uses
; TITLE OF INVENTION: Thereof for Inhibiting
; TITLE OF INVENTION: T-Cell Activation and
; TITLE OF INVENTION: Proliferation
; NUMBER OF SEQUENCES: 96
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carella, Byrne, Bain, Gilfillan,
; ADDRESSEE: Cecchi, Stewart & Olstein
; STREET: 6 Becker Farm Road
; CITY: Roseland
; STATE: New Jersey
; COUNTRY: U.S.A.
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch diskette
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 5.1

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,989B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/407,009
; FILING DATE: 29-MAR-1995
; APPLICATION NUMBER: 08/119,032
; FILING DATE: 09-SEP-1993
; APPLICATION NUMBER: 08/027,008
; FILING DATE: 05-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Olstein, Elliot M.
; REGISTRATION NUMBER: 24,025
; REFERENCE/DOCKET NUMBER: 61750-147
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 91:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 132 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: polypeptide
; FEATURE:
; NAME/KEY: Humanized LO-CD2a light chain
; NAME/KEY: variable region.

US-08-477-989B-91

Query Match 77.6%; Score 537; DB 2; Length 132;
Best Local Similarity 78.8%; Pred. No. 2.3e-44;
Matches 104; Conservative 12; Mismatches 16; Indels 0; Gaps 0;

Qy	1 MMSPAQFLFLLVLWIRETNGYVVMTQTPLTLSVTIGQPASISCKSSQSLLSDGKTYLNW	60
	: : : : :	
Db	1 MMSPVQSLFLLLWILGTNGDVVMTQSPPSLLVTLGQPASISCRSSQSLLHSSGNTYLNW	60
Qy	61 LLQRPGQSPKRLIYLVSKLDSGPDRFTGSGSGTDFTLKISREREAEDLGLYYCWQGTHFP	120
	: : : : : : : : :	
Db	61 LLQRPGQSPQPLIYLVSKEGVGPDRFSGSGSGTDFTLKISGVREAEDVGVYYCMQFTHYP	120
Qy	121 RTFGGGTKLEIK 132	
Db	121 YTFGQGTKLEIK 132	

RESULT 15

US-09-809-739-17

; Sequence 17, Application US/09809739

; Patent No. 6663863

; GENERAL INFORMATION:

; APPLICANT: Horvath, Christopher J.

; APPLICANT: Rao, Patricia E.

; TITLE OF INVENTION: Method of Inhibiting Stenosis and

; TITLE OF INVENTION: Restenosis

; FILE REFERENCE: 1855.1069-003

; CURRENT APPLICATION NUMBER: US/09/809,739
; CURRENT FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: US 09/528,267
; PRIOR FILING DATE: 2000-03-17
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized sequence
US-09-809-739-17

Query Match 77.0%; Score 533; DB 4; Length 112;
Best Local Similarity 88.3%; Pred. No. 4.6e-44;
Matches 98; Conservative 10; Mismatches 3; Indels 0; Gaps 0;

Qy 22 VVMTQTPLTLSVTIGQPASISCKSSQSLLSDGKTYLNWLLQRPGQSPKRLIYLVSKLDS 81
|||||:|||:| ||:| |||||||||||||||:|||||:|||||:|||||
Db 2 VVMTQSPSLPVLGHGPASISCKSSQSLLSDGKTFLNWLLQRPGQSPRRLIYLVSKLDS 61

Qy 82 GVPDRFTGSGSGTDFTLKISRVEAEDLGLYYCWQGTHFPRTFGGGTKLEIK 132
|||||:|||||:|||||:||||:|:|||||:|||||:|||||:|||||
Db 62 GVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCWQGTHFPYTFGGGTRLEIK 112

Search completed: May 17, 2004, 11:33:54
Job time : 17.1333 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 17, 2004, 11:25:03 ; Search time 13.2 Seconds
(without alignments)
961.915 Million cell updates/sec

Title: US-10-010-942B-2

Perfect score: 692

Sequence: 1 MMSPAQFLFLLVLWIRETNG.....CWQGTHFPRTFGGGTKLEIK 132

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR_78:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%

Result	Query				Description	
No.	Score	Match	Length	DB	ID	Description
1	678	98.0	132	2	C32513	Ig kappa chain pre
2	587	84.8	131	2	S31577	Ig kappa chain - m
3	566	81.8	113	2	F30560	Ig kappa chain V r
4	554	80.1	112	2	A55491	proteolytic antibo
5	548	79.2	112	2	A36259	ig kappa chain V r
6	547	79.0	111	2	S20709	Ig kappa chain V r
7	536	77.5	112	2	PL0273	Ig kappa chain V r
8	516	74.6	133	2	S42611	HUNVK protein prec
9	515	74.4	101	2	A33730	Ig kappa chain V r
10	515	74.4	133	2	S23230	Ig kappa chain pre
11	513	74.1	142	2	S22902	Ig kappa chain V r
12	512	74.0	133	2	S40324	Ig kappa chain V r
13	508	73.4	133	1	K2HURP	Ig kappa chain pre

14	502.5	72.6	140	2	S22658	Ig kappa chain pre
15	496	71.7	133	1	A24452	Ig kappa chain pre
16	491	71.0	132	2	S40322	Ig kappa chain - h
17	485	70.1	103	2	PH1055	Ig light chain V r
18	476	68.8	91	2	S42186	Ig kappa chain V r
19	473	68.4	120	2	S42267	Ig kappa chain V r
20	473	68.4	120	2	S42268	Ig kappa chain V r
21	470	67.9	131	2	S09259	Ig kappa chain pre
22	466	67.3	103	2	PH1056	Ig light chain V r
23	463	66.9	126	2	S40312	Ig kappa chain - h
24	463	66.9	131	2	D29380	Ig kappa chain pre
25	462.5	66.8	131	2	S40355	Ig kappa chain - h
26	462	66.8	132	2	S26882	Ig kappa chain V r
27	461.5	66.7	114	2	S49572	Ig kappa chain pre
28	460	66.5	118	2	S40374	Ig kappa chain - h
29	458.5	66.3	114	2	B49002	Ig kappa chain V r
30	458	66.2	131	2	B34904	Ig kappa chain pre
31	458	66.2	136	2	S40357	Ig kappa chain V-J
32	456	65.9	112	2	A31807	Ig kappa chain V r
33	456	65.9	131	2	B39276	Ig light chain pre
34	455	65.8	132	2	PH0106	anti-digoxin trans
35	454	65.6	131	2	C34904	Ig kappa chain pre
36	452.5	65.4	134	2	S40376	Ig kappa chain - h
37	452	65.3	122	2	S40338	Ig kappa chain - h
38	451	65.2	128	2	S40373	Ig kappa chain - h
39	450.5	65.1	130	2	S40321	Ig kappa chain - h
40	450	65.0	131	2	D34904	Ig kappa chain pre
41	450	65.0	131	2	B30577	Ig kappa chain pre
42	448	64.7	131	2	G34903	Ig kappa chain pre
43	448	64.7	135	2	S40342	Ig kappa chain - h
44	447	64.6	131	2	B32513	Ig kappa chain pre
45	446	64.5	115	2	S38715	Ig kappa chain V r

ALIGNMENTS

RESULT 1

C32513

Ig kappa chain precursor V region (BXW14) - mouse

C;Species: Mus musculus (house mouse)

C;Date: 21-May-1990 #sequence_revision 31-Dec-1990 #text_change 21-Jan-2000

C;Accession: C32513

R;Kofler, R.; Strohal, R.; Balderas, R.S.; Johnson, M.E.; Noonan, D.J.; Duchosal, M.A.; Dixon, F.J.; Theofilopoulos, A.N.

J. Clin. Invest. 82, 852-860, 1988

A;Title: Immunoglobulin kappa light chain variable region gene complex organization and immunoglobulin genes encoding anti-DNA autoantibodies in lupus mice.

A;Reference number: A94689; MUID:88331394; PMID:3138286

A;Accession: C32513

A;Molecule type: DNA

A;Residues: 1-132 <KOF>

A;Cross-references: GB:M20830; NID:g196939; PIDN:AAA38844.1; PID:g196940

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;36-115/Domain: immunoglobulin homology <IMM>

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Query Match          98.0%;  Score 678;  DB 2;  Length 132;
Best Local Similarity  97.7%;  Pred. No. 8.5e-52;
Matches 129;  Conservative 2;  Mismatches 1;  Indels 0;  Gaps 0;

Qy      1 MMSPAQFLFLLVLWIRETNGYVVMQTPLTLSVTIGQPASISCKSSQSLLSDGKTYLNW 60
       ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      1 MMSPAQFLFLLVLWIRETNGDVVMQTPLTLSVTIGQPASISCKSSQSLLSDGKTYLNW 60

Qy      61 LLQRPGQSPKRЛИYLVSKLDGVPDRFTGSGSGTDFTLKISRIEAEDLGLYYCWQGTHFP 120
       ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      61 LLQRPGQSPKRЛИYLVSKLDGVPDRFTGSGSGTDFTLKISRVEAEDLGVYYCWQGTHFP 120

Qy      121 RTFGGGTKLEIK 132
       ||||| | | | |
Db      121 RTFGGGTKLEIK 132

```

RESULT 2

S31577
Ig kappa chain - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 21-Jan-2000
C;Accession: S31577
R;Recinos, A.; Silvey, K.J.; Jensen, R.H.; Stanker, L.H.
submitted to the EMBL Data Library, January 1993
A;Description: Immunoglobulin variable heavy and light chain cDNA sequences for
two antidioxin monoclonals.
A;Reference number: S31577
A;Accession: S31577
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-131 <REC>
A;Cross-references: EMBL:Z19575; NID:g53983; PIDN:CAA79627.1; PID:g53984
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
E;35-114/Domain: immunoglobulin homology <IMM>

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Query Match          84.8%;  Score 587;  DB 2;  Length 131;
Best Local Similarity  86.3%;  Pred. No. 6.3e-44;
Matches 113;  Conservative  8;  Mismatches  10;  Indels  0;  Gaps  0;

Qy      2 MSPAQFLFLLVLWIRETNGYVVMTQTPLTLSVTIGQPASISCKSSQSLLSDGKTYLNWL 61
       |||||||:|| :|| | || || || || || :|| || || || || || || || || || || |
Db      1 MSPAQFLFLVVLSIQEINGDVVMTQAPLTLSTLGQPASISCKSSHSSLSDGKTYLNWL 60

Qy      62 LQRPGQSPKRЛИYLVSKLDGVPDRFTGSGSGTDFTLKISRВAEDLGЛYYCWWQGTHFPR 121
       |||||||:|| || || || || || || || || || || || || || || || || || || |
Db      61 LQRPGQSPKRЛИYLVSKLDGVPDRFTGSGSGTDFTLRISRВAEDLGЛYYCMQNTHFPR 120

Qy      122 TFGGGTKLEIK 132
       |||||||:|
Db      121 TFGGGTKLEMK 131

```

RESULT 3

F30560

Ig kappa chain V region (28.4.10A) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 23-Mar-1989 #sequence_revision 23-Mar-1989 #text_change 21-Jan-2000
C;Accession: F30560
R;Matsuda, T.; Kabat, E.A.
J. Immunol. 142, 863-870, 1989
A;Title: Variable region cDNA sequences and antigen binding specificity of mouse monoclonal antibodies to isomaltosyl oligosaccharides coupled to proteins. T-dependent analogues of alpha(1->6)dextran.
A;Reference number: A30560; MUID:89110062; PMID:2464028
A;Accession: F30560
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-113 <MAT>
A;Cross-references: GB:M24273; NID:g197081; PIDN:AAA63370.1; PID:g197082
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-95/Domain: immunoglobulin homology <IMM>

Query Match 81.8%; Score 566; DB 2; Length 113;
Best Local Similarity 96.4%; Pred. No. 3.5e-42;
Matches 107; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 22 VVMTQTPLTLSVTIGQPASISCKSSQSLLSDGKTYLNWLLQRPGQSPKRЛИYLVSKLDS 81
Db 2 VVMTQIPLTLSVTIGQPASISCKSSQSLLSDGKTYLNWLLQRPGQSPKRЛИYLVSKLDS 61

Qy 82 GVPDRFTGSGSGTDFTLKISRVEAEDLGLYCWQGTHFPRTFGGGTKLEIK 132
Db 62 GVPDRFTGSGSGTDFTLKISRVEAEDLGVYYCWQGTHFPHTFGGGTKLEIK 112

RESULT 4
A55491
proteolytic antibody light chain - mouse
C;Species: Mus musculus (house mouse)
C;Date: 03-Mar-1995 #sequence_revision 03-Mar-1995 #text_change 21-Jan-2000
C;Accession: A55491
R;Gao, Q.S.; Sun, M.; Tyutyulkova, S.; Webster, D.; Rees, A.; Tramontano, A.;
Massey, R.J.; Paul, S.
J. Biol. Chem. 269, 32389-32393, 1994
A;Title: Molecular cloning of a proteolytic antibody light chain.
A;Reference number: A55491; MUID:95096089; PMID:7798238
A;Accession: A55491
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-112 <GAO>
A;Cross-references: GB:L34775
A;Note: authors translated the codon TAT for residue 37 as Thr
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;16-95/Domain: immunoglobulin homology <IMM>

Query Match 80.1%; Score 554; DB 2; Length 112;
Best Local Similarity 94.6%; Pred. No. 3.8e-41;
Matches 105; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 22 VVMTQTPLTLSVTIGQPASISCKSSQSLLSDGKTYLNWLLQRPGQSPKRЛИYLVSKLDS 81

A;Residues: 1-111 <BRE>
A;Cross-references: EMBL:Z11917; NID:g52655; PIDN:CAA77975.1; PID:g52656
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-95/Domain: immunoglobulin homology <IMM>

Query Match 79.0%; Score 547; DB 2; Length 111;
Best Local Similarity 92.7%; Pred. No. 1.5e-40;
Matches 102; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

Qy 22 VVMTQTPLTLSVTIGQPASISCKSSQSLLSDGKTYLNWLLQRPGQSPKRЛИYLVSKLDS 81
: :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 2 IQLTQSPLTLSVTIGQPASISCKSSQSLLHSDGKTYLNWLLQRPGQSPKRЛИYLVSKLDS 61

Qy 82 GVPDRFTGSGSGTDFTLKISRVEAEDLGLYWCWQGTHFPRTFGGGTKLEI 131
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 62 GVPDRFTGSGSGTDFTLKISRVEAEDLGVYYCWQGTHFPQTFGGGTKLEI 111

RESULT 7

PL0273

Ig kappa chain V region (anti-DNA, D23VK) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 21-Jan-2000
C;Accession: PL0273
R;Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein, A.; Weigert, M.
J. Exp. Med. 171, 265-297, 1990
A;Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic mutation.
A;Reference number: PL0231; MUID:90111618; PMID:2104919
A;Accession: PL0273
A;Molecule type: mRNA
A;Residues: 1-112 <SHL>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-23/Region: framework 1
F;16-95/Domain: immunoglobulin homology <IMM>
F;24-39/Region: complementarity-determining 1
F;40-54/Region: framework 2
F;55-61/Region: complementarity-determining 2
F;62-93/Region: framework 3
F;94-102/Region: complementarity-determining 3
F;103-112/Region: framework 4

Query Match 77.5%; Score 536; DB 2; Length 112;
Best Local Similarity 93.7%; Pred. No. 1.4e-39;
Matches 104; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 22 VVMTQTPLTLSVTIGQPASISCKSSQSLLSDGKTYLNWLLQRPGQSPKRЛИYLVSKLDS 81
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 2 VVMTQTPLTLSVTIGQPASISCKSSQSLLYRNGKTYLNWLLQRPGQSPKRЛИYLVSKLDS 61

Qy 82 GVPDRFTGSGSGTDFTLKISRVEAEDLGLYWCWQGTHFPRTFGGGTKLEIK 132
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 62 GVPDRFTGSGSGTDFTLKISRVEAEDLGVYYCWQGTHFPWTFGGGTKLEIK 112

RESULT 8

S42611

HUNVK protein precursor - human

C;Species: Homo sapiens (man)

C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Jan-2000

C;Accession: S42611

R;Spatz, L.A.; Williams, M.; Brender, B.; Desai, R.; Latov, N.

J. Neuroimmunol. 36, 29-39, 1992

A;Title: DNA sequence analysis and comparison of the variable heavy and light chain regions of two IgM, monoclonal, anti-myelin associated glycoprotein antibodies.

A;Reference number: S42610; MUID:92138794; PMID:1370957

A;Accession: S42611

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-133 <SPA>

A;Cross-references: EMBL:X54137; NID:g433889; PIDN:CAA38072.1; PID:g433890

C;Superfamily: immunoglobulin V region; immunoglobulin homology

F;36-115/Domain: immunoglobulin homology <IMM>

Query Match	74.6%	Score 516	DB 2	Length 133;
Best Local Similarity	74.0%	Pred. No. 8.8e-38;		
Matches	97;	Conservative	16;	Mismatches 18; Indels 0; Gaps 0;

Qy 1 MMSPAQFLFLLVLWIRETNGYVVMTQTPLTLSVTIGQPASISCKSSQSLLSDGKTYLNW 60
 | |||| | ||::||: ::| |||||:||:| ||:|||||||:|||||: |||| | |||||
Db 1 MRLPAQLLGLMLWVPGSSGDVVMTQSPLSLPVTLGQPASISCRSSQSLVFSDGNTYLNW 60

Qy 61 LLQRPGQSPKRILYLVSKLDGVPDRFTGSGSGTDFTLKISRERIEADLGLYYCWQGTHFP 120
 |||||||:||||| || |||||||||:||||||| |||||:|||:||| ||| | :|:
Db 61 FQQRPGQSPRRLIYKVSNRDSGVPDRFGSGSGTDFTLKISRVEADVGIYYCMQGAHWP 120

Qy 121 RTFGGGTKLEI 131
 |||||||:|||
Db 121 LTFGGGTKEI 131

RESULT 9

A33730

Ig kappa chain V region (1.60) - mouse

C;Species: Mus musculus (house mouse)

C;Date: 09-Mar-1990 #sequence_revision 18-Sep-1992 #text_change 21-Jan-2000

C;Accession: A33730

R;Lawler, A.M.; Kearney, J.F.; Kuehl, M.; Gearhart, P.J.

Proc. Natl. Acad. Sci. U.S.A. 86, 6744-6747, 1989

A;Title: Early rearrangements of genes encoding murine immunoglobulin kappa-chains, unlike genes encoding heavy chains, use variable gene segments dispersed throughout the locus.

A;Reference number: A33730; MUID:89367325; PMID:2505260

A;Accession: A33730

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-101 <LAW>

A;Cross-references: GB:M25996; NID:g197109; PIDN:AAA38911.1; PID:g197110

A;Note: the authors translated the codon CGC for residue 51 as Leu, and TTG for residue 88 as Phe

C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-95/Domain: immunoglobulin homology <IMM>

Query Match 74.4%; Score 515; DB 2; Length 101;
Best Local Similarity 98.0%; Pred. No. 8.1e-38;
Matches 97; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 22 VVMTQTPLTLSVTIGQPASISCKSSQSLLSDGKTYLNWLLQRPGQSPKRLIYLVSKLDS 81
Db 2 VVMTQTPLTLSVTIGQPASISCKSSQSLLSDGKTYLNWLLQRPGQSPKRLIYLVSKLDS 61

Qy 82 GVPDRFTGSGSGTDFTLKISRVEAEDLGLYYCWQGTHFP 120
Db 62 GVPDRFTGSGSGTDFTLKISRVEAEDLGVYYCWQGTHFP 100

RESULT 10

S23230

Ig kappa chain precursor V-J region - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Jan-2000

C;Accession: S23230

R;Kennedy, M.A.

J. Exp. Med. 173, 1033-1036, 1991

A;Title: Novel chromosome translocation caused by fusion of immunoglobulin heavy and light chain V genes in a human B lymphoblastoid cell line.

A;Reference number: S23230; MUID:91178438; PMID:1840606

A;Accession: S23230

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-133 <KEN>

A;Cross-references: EMBL:X55400; NID:g33999; PIDN:CAA39072.1; PID:g34000

C;Genetics:

A;Introns: 17/1

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;36-115/Domain: immunoglobulin homology <IMM>

Query Match 74.4%; Score 515; DB 2; Length 133;
Best Local Similarity 74.2%; Pred. No. 1.1e-37;
Matches 98; Conservative 16; Mismatches 18; Indels 0; Gaps 0;

Qy 1 MMSPAQFLFLVLWIETNGYVVMTQTPLTLSVTIGQPASISCKSSQSLLSDGKTYLNW 60
Db 1 MRLPAQLLGLLMLWVPGSSGDVVMTQSPLSLPVTLGQPASISCRSSSQSLVYSDGNTHLNW 60

Qy 61 LLQRPGQSPKRLIYLVSKLDGSVPDRFTGSGSGTDFTLKISRVEAEDLGLYYCWQGTHFP 120
Db 61 FQQRPGQSPRRLIYKVSNRDGSVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQGTHWP 120

Qy 121 RTFGGGTKLEIK 132
Db 121 YTFGQGTKLEIK 132

RESULT 11

S22902

Ig kappa chain V region - human

C;Species: Homo sapiens (man)

C;Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000

C;Accession: S22902

R;Chastagner, P.; Theze, J.; Zouali, M.

Gene 101, 305-306, 1991

A;Title: Cloning of a gene encoding a lupus-associated human autoantibody V(K) region using the polymerase chain reaction and degenerate primers.

A;Reference number: S22902; MUID:91276289; PMID:1905262

A;Accession: S22902

A;Status: preliminary; translation not shown

A;Molecule type: mRNA

A;Residues: 1-142 <CHA>

A;Cross-references: EMBL:X56510

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;47-126/Domain: immunoglobulin homology <IMM>

Query Match 74.1%; Score 513; DB 2; Length 142;
Best Local Similarity 74.0%; Pred. No. 1.7e-37;
Matches 97; Conservative 16; Mismatches 18; Indels 0; Gaps 0;

Qy 1 MMSPAQFLFLVLWIRETNGYVVMTQTPLTSVTIGQPASISCKSSQSLLSDGKTYLNW 60
| ||| | ||:||: ::| |||||:||:| ||:|||||:||||: ||| |||||
Db 12 MRLPAQLLGMLWLVPGSSGDVVMTQSPLSLPVTLGQPASISCRSSQSLVHSDGNTYLNW 71

Qy 61 LLQRPGQSPKRLIYLVSKLDGVPDFRTGSGSGTDFTLKISRTEADLGLYYCWQGTHFP 120
||| |||:||| | ||| |||:||| ||| ||| |||:||| :||| ||| |||:
Db 72 FQQRPGQSPRRLIYKVSNRDGSVPDRFSGSGSGTDFTLKISRVEADVGVYYCMQGTHWP 131

Qy 121 RTFGGGTKLEI 131
||| |||:|||
Db 132 FTFGQGTRLEI 142

RESULT 12

S40324

Ig kappa chain V region - human

C;Species: Homo sapiens (man)

C;Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000

C;Accession: S40324

R;Klein, R.; Jaenichen, R.; Zachau, H.G.

Eur. J. Immunol. 23, 3248-3271, 1993

A;Title: Expressed human immunoglobulin chi genes and their hypermutation.

A;Reference number: S40312; MUID:94080891; PMID:8258341

A;Accession: S40324

A;Status: preliminary; translation not shown

A;Molecule type: mRNA

A;Residues: 1-133 <KLE>

A;Cross-references: EMBL:X72434

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;33-112/Domain: immunoglobulin homology <IMM>

Query Match 74.0%; Score 512; DB 2; Length 133;
Best Local Similarity 74.4%; Pred. No. 2e-37;

Matches 96; Conservative 17; Mismatches 16; Indels 0; Gaps 0;
 Qy 4 PAQFLFLLVLWIRETNGYVVMTQTPLTLSVTIGQPASISCKSSQSLLSDGKTYLNWLLQ 63
 ||| | | | : | : | | | : | | : | | | | | | : | | | : | | | | | | | | |
 Db 1 PAQLLGLLMLWVPGSSGDVVLTQSPLSLPVTIGQPASISCRSDQSLVYSDGKTYLNWYQQ 60
 Qy 64 RPGQSPKRLIYLVSKLDGVPDRFTGSGSGTDFTLKISRTEAEDLGLYYCWQGTHFPRTF 123
 || | | | : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 Db 61 RPGQSPRRLIYKVSNRDGVPDRFTGSGSGTDFTLEISRVEAEDVGVYYCMQGTHWPGT 120
 Qy 124 GGGTKLEIK 132
 | | | : | | |
 Db 121 QQGTKEIK 129

RESULT 13

K2HURP

Ig kappa chain precursor V-II region (RPMI) - human
 C;Species: Homo sapiens (man)
 C;Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 15-Aug-1997
 C;Accession: A01890
 R;Klobbeck, H.G.; Meindl, A.; Combriato, G.; Solomon, A.; Zachau, H.G.
 Nucleic Acids Res. 13, 6499-6513, 1985
 A;Title: Human immunoglobulin kappa light chain genes of subgroups II and III.
 A;Reference number: A93588; MUID:86041852; PMID:2997711
 A;Accession: A01890
 A;Molecule type: DNA
 A;Residues: 1-133 <KLO>
 A;Note: the sequence was determined from the differentiated gene
 C;Genetics:
 A;Gene: GDB:IGKV2
 A;Cross-references: GDB:136265
 A;Map position: 2p12-2p12
 A;Introns: 17/1
 C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa or lambda) and two identical heavy (alpha, delta, epsilon, gamma, or mu) chains usually stabilized by interchain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger oligomers.
 C;Superfamily: immunoglobulin V region; immunoglobulin homology
 C;Keywords: heterotetramer; immunoglobulin
 F;1-20/Domain: signal sequence #status predicted <SIG>
 F;21-133/Product: Ig kappa chain V-II region (RPMI) #status predicted <MAT>
 F;21-43/Region: framework 1
 F;36-115/Domain: immunoglobulin homology <IMM>
 F;44-59/Region: complementarity-determining 1
 F;60-74/Region: framework 2
 F;75-81/Region: complementarity-determining 2
 F;82-113/Region: framework 3
 F;114-122/Region: complementarity-determining 3
 F;123-133/Region: framework 4
 F;43-113/Disulfide bonds: #status predicted

Query Match 73.4%; Score 508; DB 1; Length 133;
 Best Local Similarity 73.5%; Pred. No. 4.3e-37;
 Matches 97; Conservative 16; Mismatches 19; Indels 0; Gaps 0;
 Qy 1 MMSPAQFLFLLVLWIRETNGYVVMTQTPLTLSVTIGQPASISCKSSQSLLSDGKTYLNW 60

Db	1	MRLPAQLLGLMLWPGSSGDVVTQSPSLPVTLGQPASISCRSSQSLVYSDGNTYLNW	60
Qy	61	LLQRPGQSPKRЛИYLVSKLDGVPDRFTGSGSGTDFTLKISR <small>EADLGLYYCWQGTHFP</small>	120
Db	61	FQQRPGQSPRRLIYKVSNRDGSVPDRFSGSGSGTDFTLKISR <small>VEADVGVYYCMQGTHWS</small>	120
Qy	121	RTFGGGTKLEIK	132
Db	121	WTFQOGTKVEIK	132

RESULT 14

S22658

Ig kappa chain precursor V region (0-81VL) - human (fragment)

C; Species: *Homo sapiens* (man)

C:\Date: 29-Jan-1998 #sequence revision 06-Feb-1998 #text_change 21-Jan-2000

C:Accession: S22658

R:Hirabayashi, Y.; Munakata, Y.; Sasaki, T.; Sano, H.

Nucleic Acids Res. 20, 2601, 1992

A;Title: Variable regions of a human anti-DNA antibody O-81 possessing lupus nephritis-associated idiotype.

A:Reference number: S22657; MUID:92285150; PMID:1598223

A:Accession: S22658

A, Accession: B22050

A; Molecule type: mRNA

► Cross-references: EMBL:X58135

A; cross-references: EMBL: X50135

C; Superfamily: immunoglobulin V region; Immature protein: heterotrimeric immunoglobulin

C;Keywords: heterotetramer; immunoglobulin

F;1-19/Domain: signal sequence #status predicted <SIG>

F;20-140/Product: Ig kappa chain (fragment) #status predicted <MAP>
F;36-115/Domain: immunoglobulin homology <IMM>

```

Query Match                72.6%;  Score 502.5;  DB 2;  Length 140;
Best Local Similarity    73.7%;  Pred. No. 1.4e-36;
Matches      98;  Conservative   15;  Mismatches     19;  Indels       1;  Gaps        1;

Qy          1 MMSPAQFLFLLVLWIRETNGYVVMTQTPLTLSVTIGQPASISCKSSQSLLSDGKTYLNW 60
           | ||||| | ||::||: ::| |||||||:|||: |||:|||||||:|||||: ||| |||||
Db          1 MRLPAQLLGLLMLWPGSSGDVVMTQSPLSLPVTLGQPASISCRSSQSLVHSDGNTYLNW 60

Qy          61 LLQRPGQSPKRЛИYLVSKLDGVPDRFTGSGSGTDFTLKISRIVEAEDLGLYYCWQGTHF- 119
           |||||||:||| | ||| |||||||||:|||||||:|||||:|||||: ||| |
Db          61 FQQRPGQSPRRLIYRVSNRDGVPDRFSGSGSGTDFTLKISRVEAEDVGLYYCMQHTHWS 120

Qy          120 PRTFGGGTKLEIK 132
           | ||| | ||:|||
Db          121 PITFGQQGTRLEIK 133

```

RESULT 15

A24452

Ig kappa chain precursor V-II region (RPMI 6410) - human

C:Species: *Homo sapiens* (man)

C:Date: 24-Jan-1988 #sequence revision 09-Aug-1996 #text_change 16-Jul-1999

C:\Accession: A24452

C, ACCESSION: REVERSE
B:Weir, L.: Leder, P.

Nucleic Acids Res. 14, 3957-3970, 1986

Nucleic Acids Res. 19, 101-111, 1991.
A;Title: Structure and expression of a human subgroup II immunoglobulin kappa gene.

A; Reference number: A24452; MUID:86232631; PMID:3086847

A; Accession: A24452

A: Molecule type: DNA

A:Residues: 1-133 <WEI>

A:Cross-references: GB:M36859; NID:g185932; PIDN:AAA58920.1; PID:g185933

A:Note: this sequence was determined from the differentiated gene

A, NOCC
S. Sene

A:Gene: GDB: TGKV2

A;Cross references: GDB:136265

A; Cross-references: GDB:1

A; Map position:
A. Entrepeneur: 17/1

C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa or lambda) and two identical heavy (alpha, delta, epsilon, gamma, or mu) chains usually stabilized by interchain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger oligomers.

C: Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

E-1 22/Domain: signal sequence #status predicted <SIG>

F;1-20/Domain: signal sequence #status predicted <MAT>
E;21_33/Product: Ig kappa chain V-II region (RPMI 6410) #status predicted <MAT>

B-26-115/Domain: immunoglobulin homology <IMM>

F;36-115/Domain: Immunoglobulin homology, C-terminal
E;43-113/Sulfide bonds: #status predicted

Query Match 71.7%; Score 496; DB 1; Length 133;
Best Local Similarity 72.7%; Pred. No. 4.7e-36;
Matches 86; Conservative 15; Mismatches 21; Indels 0; Gaps 0;

QY 1 MMSPAQFLFLLVLWIRETNGYVVMTQTPLTLSVTIGQPASISCKSSQSLLSDGKTYLNW 60

1 MRLPAOALLGLLRLWPGSSGVDVVMTQSPLSLPVTLGQPASISCRSSQSLVYSDRNTYLNW 60

61 FQQRPGQS^PRRLIYKVSNRDGVPDRFSGSGSTDFTLKISRVEAE^DVGVYYCMQGTHWS 120

Qy 121 RTFGGGTKLEIK 132

||| : |||

Db 121 WTFGQQGTVKVEIK 132

Search completed: May 17, 2004, 11:33:08

Job time : 13.2 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 17, 2004, 11:32:34 ; Search time 37.6444 Seconds
(without alignments)
975.722 Million cell updates/sec

Title: US-10-010-942B-2
Perfect score: 692
Sequence: 1 MMSPAQFLFLLVLWIRETNG.....CWQGTHFPRTFGGGTKLEIK 132

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1145568 seqs, 278261457 residues

Total number of hits satisfying chosen parameters: 1145568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:
1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%

Result	Query				
No.	Score	Match	Length	DB	ID
					Description

1	692	100.0	132	14	US-10-010-942B-2	Sequence 2, Appli
2	692	100.0	132	16	US-10-388-389-2	Sequence 2, Appli
3	650	93.9	135	9	US-09-881-823-10	Sequence 10, Appli
4	649	93.8	131	12	US-10-462-062-163	Sequence 163, App
5	646	93.4	131	12	US-10-462-062-164	Sequence 164, App
6	640	92.5	132	14	US-10-010-942B-5	Sequence 5, Appli
7	640	92.5	132	16	US-10-388-389-5	Sequence 5, Appli
8	636	91.9	132	13	US-10-006-773-11	Sequence 11, Appli
9	630	91.0	132	14	US-10-010-942B-11	Sequence 11, Appli
10	630	91.0	132	16	US-10-388-389-11	Sequence 11, Appli
11	606	87.6	142	9	US-09-840-459-102	Sequence 102, App
12	560	80.9	112	9	US-09-835-087-1	Sequence 1, Appli
13	560	80.9	112	9	US-09-809-739-11	Sequence 11, Appli
14	560	80.9	112	9	US-09-840-459-9	Sequence 9, Appli
15	560	80.9	122	12	US-10-272-899A-86	Sequence 86, Appli
16	560	80.9	130	12	US-10-272-899A-88	Sequence 88, Appli
17	559	80.8	112	12	US-10-462-062-149	Sequence 149, App
18	559	80.8	112	12	US-10-462-062-150	Sequence 150, App
19	556	80.3	112	9	US-09-840-459-54	Sequence 54, Appli
20	551	79.6	500	14	US-10-168-809-22	Sequence 22, Appli
21	548	79.2	112	9	US-09-772-120-6	Sequence 6, Appli
22	548	79.2	535	9	US-09-968-851-38	Sequence 38, Appli
23	547	79.0	162	15	US-10-410-907A-30	Sequence 30, Appli
24	546	78.9	112	15	US-10-323-903-1	Sequence 1, Appli
25	538	77.7	112	9	US-09-835-087-5	Sequence 5, Appli
26	538	77.7	112	9	US-09-809-739-16	Sequence 16, Appli
27	538	77.7	112	9	US-09-840-459-14	Sequence 14, Appli
28	533	77.0	112	9	US-09-835-087-6	Sequence 6, Appli
29	533	77.0	112	9	US-09-809-739-17	Sequence 17, Appli
30	533	77.0	112	9	US-09-840-459-15	Sequence 15, Appli
31	530	76.6	112	9	US-09-835-087-4	Sequence 4, Appli
32	530	76.6	112	9	US-09-809-739-15	Sequence 15, Appli
33	530	76.6	112	9	US-09-840-459-13	Sequence 13, Appli
34	527	76.2	114	9	US-09-840-459-106	Sequence 106, App
35	526	76.0	112	13	US-10-032-482-8	Sequence 8, Appli
36	525	75.9	112	9	US-09-835-087-7	Sequence 7, Appli
37	525	75.9	112	9	US-09-809-739-18	Sequence 18, Appli
38	525	75.9	112	9	US-09-840-459-107	Sequence 107, App
39	520	75.1	112	9	US-09-835-087-3	Sequence 3, Appli
40	520	75.1	112	9	US-09-809-739-14	Sequence 14, Appli
41	520	75.1	112	9	US-09-840-459-12	Sequence 12, Appli
42	515	74.4	100	9	US-09-840-459-22	Sequence 22, Appli
43	511	73.8	132	15	US-10-309-764-117	Sequence 117, App
44	510	73.7	132	15	US-10-309-764-113	Sequence 113, App
45	506	73.1	132	15	US-10-309-764-109	Sequence 109, App

ALIGNMENTS

RESULT 1

US-10-010-942B-2
; Sequence 2, Application US/10010942B
; Publication No. US20030165496A1
; GENERAL INFORMATION:
; APPLICANT: Basi, Guriq

; APPLICANT: Saldanha, Jose
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE
; TITLE OF INVENTION: BETA AMYLOID PEPTIDE
; FILE REFERENCE: ELN-002
; CURRENT APPLICATION NUMBER: US/10/010,942B
; CURRENT FILING DATE: 2002-12-06
; PRIOR APPLICATION NUMBER: US 60/251,892
; PRIOR FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)...(20)

US-10-010-942B-2

Query Match 100.0%; Score 692; DB 14; Length 132;
Best Local Similarity 100.0%; Pred. No. 4.1e-59;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MMSPAQFLFLLVLWIRETNGYVVMTQTPLTLSVTIGQPASISCKSSQSLLSDGKTYLNW 60
Db |||||||
Qy 1 MMSPAQFLFLLVLWIRETNGYVVMTQTPLTLSVTIGQPASISCKSSQSLLSDGKTYLNW 60
Db |||||||
Qy 61 LLQRPGQSPKRЛИYLVSKLDGVPDRFTGSGSGTDFTLKISRIEAEDLGLYYCWQGTHFP 120
Db |||||||
Qy 61 LLQRPGQSPKRЛИYLVSKLDGVPDRFTGSGSGTDFTLKISRIEAEDLGLYYCWQGTHFP 120
Db |||||||
Qy 121 RTFGGGTKLEIK 132
Db |||||||
Db 121 RTFGGGTKLEIK 132

RESULT 2

US-10-388-389-2

; Sequence 2, Application US/10388389
; Publication No. US20040087777A1
; GENERAL INFORMATION:
; APPLICANT: Basi, Guriq
; APPLICANT: Saldanha, Jose
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE
; TITLE OF INVENTION: BETA-AMYLOID PEPTIDE
; FILE REFERENCE: ELN-002CP
; CURRENT APPLICATION NUMBER: US/10/388,389
; CURRENT FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: US 10/010,942
; PRIOR FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: US 60/251,892
; PRIOR FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2

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; LENGTH: 132
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)...(20)
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US-10-388-389-2

RESULT 3

US-09-881-823-10

; Sequence 10, Application US/09881823
; Patent No. US20020068066A1
; GENERAL INFORMATION:
; APPLICANT: SHI, WENYUAN
; APPLICANT: ANDERSON, MAXWELL
; APPLICANT: MORRISON, SHERIE
; APPLICANT: TRINH, RYAN
; APPLICANT: WIMS, LETITIA
; APPLICANT: CHEN, LI
; TITLE OF INVENTION: Method for the Treatment and Prevention of Dental Caries
; FILE REFERENCE: 22851-032
; CURRENT APPLICATION NUMBER: US/09/881,823
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: US 07/378,577
; PRIOR FILING DATE: 1999-08-20
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 10
; LENGTH: 135
; TYPE: PRT
; ORGANISM: Murine
US-09-881-823-10

US-09-881-823-10

```

Qy      61 LLQPGQSPKRLIYLVSKLDGVPDRFTGSGSGTDFTLKISRVEAEDLGLYYCWQGTHFP 120
       |||||||:|||||||:|||||||:|||||||:|||||||:|||||||:|||||||:|||||||:|
Db      61 LLQPGQSPKRLIYLVSKLDGVPDRFTGSGSGTDFTLKISRVEAEDLGVYYCWQGTHFP 120

Qy      121 RTFGGGTKLEIK 132
       ||| | | | |:|
Db      121 LTFGAGTKLELK 132

```

RESULT 4

US-10-462-062-163

; Sequence 163, Application US/10462062
; Publication No. US20040044187A1
; GENERAL INFORMATION:
; APPLICANT: SATO, KOH
; APPLICANT: ADACHI, HIDEKI
; TITLE OF INVENTION: HUMANIZED ANTIBODIES AGAINST HUMAN TISSUE FACTOR (TF)
; TITLE OF INVENTION: AND PROCESS OF PRODUCTION OF THE HUMANIZED ANTIBODIES
; FILE REFERENCE: 053466-0360
; CURRENT APPLICATION NUMBER: US/10/462,062
; CURRENT FILING DATE: 2003-06-16
; PRIOR APPLICATION NUMBER: PCT/JP99/01768
; PRIOR FILING DATE: 1999-04-02
; PRIOR APPLICATION NUMBER: JP 10-91850
; PRIOR FILING DATE: 1998-04-03
; NUMBER OF SEQ ID NOS: 183
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 163
; LENGTH: 131
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Full-length amino acid
; OTHER INFORMATION: sequence for L chain V region of anti-TF mouse monoclonal
; OTHER INFORMATION: antibody ATR-7

US-10-462-062-163

Query Match 93.8%; Score 649; DB 12; Length 131;
Best Local Similarity 93.9%; Pred. No. 5.7e-55;
Matches 123; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

```

Qy      2 MSPAQFLFLLVLWIRETNGYVVMTQTPLTLSVTIGQPASISCKSSQSLLSDGKTYLNWL 61
       |||||||:|||||||:|||||||:|||||||:|||||||:|||||||:|||||||:|||||||:|
Db      1 MSPAQFLFLLVLWIREINGDVVLQTPLTLSVTIGQPASVSKSSQSLLSDGKTYLNWL 60

Qy      62 LQRPGQSPKRLIYLVSKLDGVPDRFTGSGSGTDFTLKISRVEAEDLGLYYCWQGTHFPR 121
       |||||||:|||||||:|||||||:|||||||:|||||||:|||||||:|||||||:|||||||:|
Db      61 LQRPGQSPKRLIYLVSKLDGVPDRFTGSGSGTDFTLKISRVEAEDLGVYYCWQDTHFPD 120

Qy      122 TFGGGTKEIK 132
       ||| | | | | |
Db      121 TFGGGTKEIK 131

```

RESULT 5

US-10-462-062-164
; Sequence 164, Application US/10462062
; Publication No. US20040044187A1
; GENERAL INFORMATION:
; APPLICANT: SATO, KOH
; APPLICANT: ADACHI, HIDEKI
; TITLE OF INVENTION: HUMANIZED ANTIBODIES AGAINST HUMAN TISSUE FACTOR (TF)
; TITLE OF INVENTION: AND PROCESS OF PRODUCTION OF THE HUMANIZED ANTIBODIES
; FILE REFERENCE: 053466-0360
; CURRENT APPLICATION NUMBER: US/10/462,062
; CURRENT FILING DATE: 2003-06-16
; PRIOR APPLICATION NUMBER: PCT/JP99/01768
; PRIOR FILING DATE: 1999-04-02
; PRIOR APPLICATION NUMBER: JP 10-91850
; PRIOR FILING DATE: 1998-04-03
; NUMBER OF SEQ ID NOS: 183
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 164
; LENGTH: 131
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Full-length amino acid
; OTHER INFORMATION: sequence for L chain V region of anti-TF mouse monoclonal
; OTHER INFORMATION: antibody ATR-8

US-10-462-062-164

Query Match 93.4%; Score 646; DB 12; Length 131;
Best Local Similarity 93.1%; Pred. No. 1.1e-54;
Matches 122; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy 2 MSPAQFLFLLVLWIRETNGYVVMQTPLTLSVTIGQPASISCKSSQSLLSDGKTYLNWL 61
||| ||| ||| ||| : || | : ||| ||| ||| ||| : ||| ||| ||| |||
Db 1 MSPAQFLFLLVLWIRDINGDVVLQTPLTLSVTIGQPASVSCKSSQSLLSDGKTYLNWL 60

Qy 62 LQRPGQSPKRЛИYLVSKLDSGVPDFRTGSGSGTDFTLKISRVEAEDLGLYYCWQGTHFPR 121
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| : ||| ||| : ||| |||
Db 61 LQRPGQSPKRЛИYLVSKLDSGVPDFRTGSGSGTDFTLKISRVEAEDLGVYYCWQDTHFPD 120

Qy 122 TFGGGTKEIK 132
||| ||| ||| |||
Db 121 TFGGGTKEIK 131

RESULT 6

US-10-010-942B-5

; Sequence 5, Application US/10010942B
; Publication No. US20030165496A1
; GENERAL INFORMATION:
; APPLICANT: Basi, Guriq
; APPLICANT: Saldanha, Jose
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE
; TITLE OF INVENTION: BETA AMYLOID PEPTIDE
; FILE REFERENCE: ELN-002
; CURRENT APPLICATION NUMBER: US/10/010,942B

; CURRENT FILING DATE: 2002-12-06
; PRIOR APPLICATION NUMBER: US 60/251,892
; PRIOR FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: FastSEQ for Windows Version 4.0
;
SEQ ID NO 5
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Artificial Sequence
;
FEATURE:
;
NAME/KEY: SIGNAL
;
LOCATION: (1)...(20)
;
OTHER INFORMATION: humanized 3D6 light chain variable region
US-10-010-942B-5

Query Match 92.5%; Score 640; DB 14; Length 132;
Best Local Similarity 90.2%; Pred. No. 4.3e-54;
Matches 119; Conservative 10; Mismatches 3; Indels 0; Gaps 0;

Qy	1	MMSPAQFLFLLVLWIRETNGYVVMQTPLTLSVTIGQPASISCKSSQSLLSDGKTYLNW	60
Db	1	MMSPAQFLFLLVLWIRETNGYVVMTQSPLSLPVTGPAPASISCKSSQSLLSDGKTYLNW	60
Qy	61	LLQRPGQSPKRLIYLVSKLDGVPDRFTGSGSGTDFTLKISRVEAEDLGLYYCWQGTHFP	120
Db	61	LLQKPGQSPQRLIYLVSKLDGVPDRFTGSGSGTDFTLKISRVEAEDVGVYYCWQGTHFP	120
Qy	121	RTFGGGTKLEIK 132	
Db	121	RTFGQGTKVEIK 132	

RESULT 7

US-10-388-389-5
; Sequence 5, Application US/10388389
; Publication No. US20040087777A1
; GENERAL INFORMATION:
; APPLICANT: Basi, Guriq
; APPLICANT: Saldanha, Jose
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE
; TITLE OF INVENTION: BETA-AMYLOID PEPTIDE
; FILE REFERENCE: ELN-002CP
; CURRENT APPLICATION NUMBER: US/10/388,389
; CURRENT FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: US 10/010,942
; PRIOR FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: US 60/251,892
; PRIOR FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: SIGNAL

; LOCATION: (1)...(20)
; OTHER INFORMATION: humanized 3D6 light chain variable region
US-10-388-389-5

Query Match 92.5%; Score 640; DB 16; Length 132;
Best Local Similarity 90.2%; Pred. No. 4.3e-54;
Matches 119; Conservative 10; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MMSPAQFLFLLVLWIRETNGYVVMTQTPLTLSVTIGQPASISCKSSQSLLSDGKTYLNW 60
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 MMSPAQFLFLLVLWIRETNGYVVMTQSPLSLPVTPGEPASISCKSSQSLLSDGKTYLNW 60

Qy 61 LLQRPQSPKRLIYLVSKLDGVPDFRTGSGSGTDFTLKISRTEAEDLGLYYCWQGTHFP 120
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 LLQKPGQSPQRLLIYLVSKLDGVPDFRTGSGSGTDFTLKISRVEAEDVGVYYCWQGTHFP 120

Qy 121 RTFGGGTKLEIK 132
|||:|||||:
Db 121 RTFGQGTKVEIK 132

RESULT 8
US-10-006-773-11
; Sequence 11, Application US/10006773
; Publication No. US20020132983A1
; GENERAL INFORMATION:
; APPLICANT: Junghans, Richard P.
; TITLE OF INVENTION: Antibodies as Chimeric Effector Cell Receptors Against Tumor Antigens
; FILE REFERENCE: 003
; CURRENT APPLICATION NUMBER: US/10/006,773
; CURRENT FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: 60/250,089
; PRIOR FILING DATE: 2000-11-30
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Mus sp.
US-10-006-773-11

Query Match 91.9%; Score 636; DB 13; Length 132;
Best Local Similarity 93.9%; Pred. No. 1e-53;
Matches 123; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 2 MSPAQFLFLLVLWIRETNGYVVMTQTPLTLSVTIGQPASISCKSSQSLLSDGKTYLNWL 61
|||:|||||:|||||:|||||:|||||:|||||:
Db 1 MSPAQFLFLLVLWIQETNGDVVMTQTPLTLSVTIGQPASISCKSSQSLLYSNGKTYLNWL 60

Qy 62 LQRPQSPKRLIYLVSKLDGVPDFRTGSGSGTDFTLKISRTEAEDLGLYYCWQGTHFPR 121
|||:|||||:|||||:|||||:|||||:
Db 61 LQRPQSPKRLIYLVSKLDGVPDFRTGSGSGTDFTLKISRVEAEDLGVYYCVQGTHFPH 120

Qy 122 TFGGGTKEIK 132
|||:|||||:
Db 121 TFGGGTKEIK 131

RESULT 9
US-10-010-942B-11
; Sequence 11, Application US/10010942B
; Publication No. US20030165496A1
; GENERAL INFORMATION:
; APPLICANT: Basi, Guriq
; APPLICANT: Saldanha, Jose
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE
; TITLE OF INVENTION: BETA AMYLOID PEPTIDE
; FILE REFERENCE: ELN-002
; CURRENT APPLICATION NUMBER: US/10/010,942B
; CURRENT FILING DATE: 2002-12-06
; PRIOR APPLICATION NUMBER: US 60/251,892
; PRIOR FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)...(20)
; OTHER INFORMATION: humanized 3D6 light chain variable region
US-10-010-942B-11

Query Match 91.0%; Score 630; DB 14; Length 132;
Best Local Similarity 89.4%; Pred. No. 3.9e-53;
Matches 118; Conservative 10; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MMSPAQFLFLLVLWIRETNGYVVMTQTPLTLSVTIGQPASISCKSSQSLLSDGKTYLNW 60
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 MMSPAQFLFLLVLWIRETNGDVVMTQSPLSLPVTPGEPASISCKSSQSLLSDGKTYLNW 60

Qy 61 LLQRPGQSPKRЛИYLVSKLDGVPDFRGSGSGTDFTLKISRRIEADLGLYYCWQGTHFP 120
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 LLQKPGQSPQRЛИYLVSKLDGVPDFRGSGSGTDFTLKISRVEAEDVGVYYCWQGTHFP 120

Qy 121 RTFGGGTKLEIK 132
|||||:|||||
Db 121 RTFGQGTKVEIK 132

RESULT 10
US-10-388-389-11
; Sequence 11, Application US/10388389
; Publication No. US20040087777A1
; GENERAL INFORMATION:
; APPLICANT: Basi, Guriq
; APPLICANT: Saldanha, Jose
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE
; TITLE OF INVENTION: BETA-AMYLOID PEPTIDE
; FILE REFERENCE: ELN-002CP

; CURRENT APPLICATION NUMBER: US/10/388,389
; CURRENT FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: US 10/010,942
; PRIOR FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: US 60/251,892
; PRIOR FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)...(20)
; OTHER INFORMATION: humanized 3D6 light chain variable region
US-10-388-389-11

Query Match 91.0%; Score 630; DB 16; Length 132;
Best Local Similarity 89.4%; Pred. No. 3.9e-53;
Matches 118; Conservative 10; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MMSPAQFLFLLVLWIRETNGYVVMTQTPLTLSVTIGQPASISCKSSQSLLSDGKTYLNW 60
Db |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 61 LLQRPGQSPKRLIYLVSKLDGVPDFRGSGSGTDFTLKISRVEAEDLGLYYCWQGTHFP 120
Db 61 LLQKPGQSPQRLIYLVSKLDGVPDFRGSGSGTDFTLKISRVEAEDVGVYYCWQGTHFP 120
Qy 121 RTFGGGTKLEIK 132
Db ||||| |||:|||
Do 121 RTFGQGTKVEIK 132

RESULT 11

US-09-840-459-102
; Sequence 102, Application US/09840459
; Patent No. US20020150576A1
; GENERAL INFORMATION:
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; TITLE OF INVENTION: METHODS OF USE THEREFOR
; FILE REFERENCE: 1855.1052-012
; CURRENT APPLICATION NUMBER: US/09/840,459
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: PCT/US01/03537
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22

; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 102
; LENGTH: 142
; TYPE: PRT
; ORGANISM: Mus musculus

US-09-840-459-102

Query Match 87.6%; Score 606; DB 9; Length 142;
Best Local Similarity 93.5%; Pred. No. 8.9e-51;
Matches 115; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 10 LLVLWIRETNGYVVMTQTPLTLSVTIGQPASISCKSSQSLLSDGKTYLNWLQRPGQSP 69
Db 7 LLVLWIRETIGDVVMTQTPLTLSVTVGHPASISCKSSQSLLSDGKTFLNWLLQRPGQSP 66

Qy 70 KRLIYLVSKLDSGVPDFRTGSGSGTDFTLKISRVEAEDLGLYYCWQGTHFPRTFGGGTKL 129
Db 67 KRLIYLVSKLDSGVPDFRTGSGSGTDFTLKISRVEAEDLGVYYCWQGTHFPYTFGGGTKL 126

Qy 130 EIK 132
Db 127 EIK 129

RESULT 12

US-09-835-087-1

; Sequence 1, Application US/09835087
; Patent No. US20020042370A1
; GENERAL INFORMATION:
; APPLICANT: Wayne W. Hancock
; TITLE OF INVENTION: Method of Treating Graft Rejection Using
; TITLE OF INVENTION: Inhibitors of CCR2 Function
; FILE REFERENCE: 1855.2008-003
; CURRENT APPLICATION NUMBER: US/09/835,087
; CURRENT FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: 09/549,448
; PRIOR FILING DATE: 2000-04-14
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Mus Musculus
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (1)...(112)
; OTHER INFORMATION: Murine mAb 1D9 light chain variable region

US-09-835-087-1

Query Match 80.9%; Score 560; DB 9; Length 112;
Best Local Similarity 94.6%; Pred. No. 1.9e-46;
Matches 105; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 22 VVMTQTPLTLSVTIGQPASISCKSSQSLLSDGKTYLNWLQRPGQSPKRLIYLVSKLDS 81

Db 2 VVMTQTPLTLSVTVGHPASISCKSSQSLLSDGKTFLNWLLQRPGQSPKRЛИYLVSKLDS 61
Qy 82 GVPDRFTGSGSGTDFTLKISRIEAEDLGLYYCWQGTHFPRTFGGGTKLEIK 132
Db 62 GVPDRFTGSGSGTDFTLKISRVEAEDLGVYYCWQGTHFPYTFFGGTKLEIK 112

RESULT 13

US-09-809-739-11

; Sequence 11, Application US/09809739
; Patent No. US20020106369A1
; GENERAL INFORMATION:
; APPLICANT: Horvath, Christopher J.
; APPLICANT: Rao, Patricia E.
; TITLE OF INVENTION: Method of Inhibiting Stenosis and
; TITLE OF INVENTION: Restenosis
; FILE REFERENCE: 1855.1069-003
; CURRENT APPLICATION NUMBER: US/09/809,739
; CURRENT FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: US 09/528,267
; PRIOR FILING DATE: 2000-03-17
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1)...(112)
; OTHER INFORMATION: Murine mAb 1D9 light chain variable region
; NAME/KEY: SITE
; LOCATION: (24)...(39)
; OTHER INFORMATION: CDR1
; NAME/KEY: SITE
; LOCATION: (55)...(61)
; OTHER INFORMATION: CDR2
; NAME/KEY: SITE
; LOCATION: (94)...(102)
; OTHER INFORMATION: CDR3
; OTHER INFORMATION: Mouse

US-09-809-739-11

Query Match 80.9%; Score 560; DB 9; Length 112;
Best Local Similarity 94.6%; Pred. No. 1.9e-46;
Matches 105; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 22 VVMTQTPLTLSVTIGQPASISCKSSQSLLSDGKYLNWLLQRPGQSPKRЛИYLVSKLDS 81
Db 2 VVMTQTPLTLSVTVGHPASISCKSSQSLLSDGKTFLNWLLQRPGQSPKRЛИYLVSKLDS 61
Qy 82 GVPDRFTGSGSGTDFTLKISRIEAEDLGLYYCWQGTHFPRTFGGGTKLEIK 132
Db 62 GVPDRFTGSGSGTDFTLKISRVEAEDLGVYYCWQGTHFPYTFFGGTKLEIK 112

RESULT 14

US-09-840-459-9

; Sequence 9, Application US/09840459
; Patent No. US20020150576A1
; GENERAL INFORMATION:
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; TITLE OF INVENTION: METHODS OF USE THEREFOR
; FILE REFERENCE: 1855.1052-012
; CURRENT APPLICATION NUMBER: US/09/840,459
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: PCT/US01/03537
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Mus musculus

US-09-840-459-9

Query Match 80.9%; Score 560; DB 9; Length 112;
Best Local Similarity 94.6%; Pred. No. 1.9e-46;
Matches 105; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 22 VVMTQTPLTLSVTIGQPASISCKSSQSLSDGKTYLNWLLQRPGQSPKRЛИYLVSKLDS 81
Db 2 VVMTQTPLTLSVTVGHPASISCKSSQSLSDGKTFLNWLLQRPGQSPKRЛИYLVSKLDS 61

Qy 82 GVPDRFTGSGSGTDFTLKISRRIEAEDLGLYYCWQGTHFPRTFGGGTKLEIK 132
Db 62 GVPDRFTGSGSGTDFTLKISRVEAEDLGVYYCWQGTHFPYTFGGGTKEIK 112

RESULT 15

US-10-272-899A-86

; Sequence 86, Application US/10272899A
; Publication No. US20040033561A1
; GENERAL INFORMATION:
; APPLICANT: O'Keefe, Theresa L.
; APPLICANT: Healy, Judith Jacques
; APPLICANT: Newman, Walter
; APPLICANT: Ponath, Paul
; APPLICANT: Bruce Keyt
; TITLE OF INVENTION: IMMUNOGLOBULIN DNA CASSETTE MOLECULES,

; TITLE OF INVENTION: MONOBODY CONSTRUCTS, METHODS OF PRODUCTION, AND METHODS
OF
; TITLE OF INVENTION: USE THEREFOR
; FILE REFERENCE: MPI01-244P2RM
; CURRENT APPLICATION NUMBER: US/10/272,899A
; CURRENT FILING DATE: 2002-10-17
; PRIOR APPLICATION NUMBER: 60/350,166
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: 60/392,364
; PRIOR FILING DATE: 2002-06-26
; NUMBER OF SEQ ID NOS: 110
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 86
; LENGTH: 122
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: variable insert protein sequence n1D9VK hum
US-10-272-899A-86

Query Match 80.9%; Score 560; DB 12; Length 122;
Best Local Similarity 94.6%; Pred. No. 2.1e-46;
Matches 105; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 22 VVMTQTPLTLSVTIGQPASISCKSSQSLLSDGKTYLNWLLQRPGQSPKRLIYLVSKLDS 81
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 8 VVMTQTPLTLSVTVGHPASISCKSSQSLLSDGKTFLNWLLQRPGQSPKRLIYLVSKLDS 67

Qy 82 GVPDRFTGSGSGTDFTLKISRVEAEDLGLYYCWQGTHFPRTFGGGTKLEIK 132
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 68 GVPDRFTGSGSGTDFTLKISRVEAEDLGVYYCWQGTHFPYTFGGGTKEIK 118

Search completed: May 17, 2004, 11:42:05
Job time : 38.6444 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 17, 2004, 11:25:03 ; Search time 13.8 Seconds
(without alignments)
961.915 Million cell updates/sec

Title: US-10-010-942B-4

Perfect score: 719

Sequence: 1 MNFGLSLIFLVLVLKGQCE.....DHYSGSSDYWGQGTTVTVSS 138

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR_78:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%

Result No.	Query Score	Match	Length	DB	ID	Description
1	573	79.7	138	2	S09258	Ig heavy chain V r
2	569	79.1	152	2	B26471	Ig heavy chain pre
3	559.5	77.8	139	2	S38808	Ig heavy chain - m
4	544	75.7	142	2	C34903	Ig heavy chain pre
5	521.5	72.5	140	2	S70442	Ig heavy chain pre
6	517	71.9	140	2	S31686	Ig heavy chain V r
7	516	71.8	160	2	S05271	Ig heavy chain pre
8	514	71.5	134	2	S31699	Ig heavy chain V r
9	513	71.3	140	2	S31588	Ig heavy chain V r
10	512	71.2	117	1	HVMS84	Ig heavy chain pre
11	510	70.9	117	1	HVMS34	Ig heavy chain pre
12	508	70.7	136	2	S31615	hypothetical prote
13	504	70.1	140	2	S22657	Ig heavy chain pre

14	502.5	69.9	136	1	G1MS21	Ig heavy chain pre
15	502	69.8	138	2	S31666	Ig heavy chain V r
16	501	69.7	117	1	HVMS39	Ig heavy chain pre
17	495	68.8	135	2	S31598	Ig heavy chain V r
18	493	68.6	134	2	S31679	Ig heavy chain V r
19	492.5	68.5	141	2	S31669	Ig heavy chain V r
20	492	68.4	117	1	HVMSRF	Ig heavy chain pre
21	492	68.4	139	2	I37781	Ig variable region
22	490	68.2	122	2	E27888	Ig heavy chain V r
23	487.5	67.8	119	2	F27888	Ig heavy chain V r
24	485.5	67.5	136	2	S31587	Ig heavy chain V r
25	484.5	67.4	151	2	A60943	Ig heavy chain pre
26	484	67.3	117	1	HVMS57	Ig heavy chain pre
27	484	67.3	140	2	A30532	Ig heavy chain pre
28	483	67.2	120	2	S55536	Ig heavy chain V r
29	481.5	67.0	147	2	I37780	Ig variable region
30	480.5	66.8	118	2	PH0096	Ig heavy chain V r
31	480.5	66.8	121	2	S55540	Ig heavy chain V r
32	480.5	66.8	254	2	B31790	Ig heavy chain V r
33	479	66.6	120	2	S55538	Ig heavy chain V r
34	479	66.6	120	2	S55539	Ig heavy chain V r
35	477.5	66.4	121	2	H27888	Ig heavy chain V r
36	477.5	66.4	137	2	S31701	Ig heavy chain V r
37	477.5	66.4	139	2	S31674	Ig heavy chain V r
38	476.5	66.3	137	2	S78054	Ig heavy chain pre
39	476	66.2	120	2	S55537	Ig heavy chain V r
40	473.5	65.9	118	2	PH0097	Ig heavy chain V r
41	472	65.6	132	2	S31603	Ig heavy chain V r
42	471	65.5	130	2	PL0098	Ig heavy chain pre
43	469	65.2	118	2	S20641	Ig heavy chain V r
44	467.5	65.0	135	2	I37778	Ig variable region
45	467.5	65.0	145	2	S11239	Ig heavy chain V r

ALIGNMENTS

RESULT 1

S09258

Ig heavy chain V region precursor - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 29-Jan-1993 #sequence_revision 29-Jan-1993 #text_change 23-Jul-1999

C;Accession: S09258

R;Hamada, H.; Maezawa, K.; Tsuruo, T.

Nucleic Acids Res. 18, 1900, 1990

A;Title: Nucleotide sequences of the variable regions of a mouse monoclonal antibody MRK16.

A;Reference number: S09258; MUID:90245594; PMID:2110659

A;Accession: S09258

A;Molecule type: DNA

A;Residues: 1-138 <HAM>

A;Cross-references: EMBL:X51719; NID:g53207; PIDN:CAA36012.1; PID:g297545

C;Genetics:

A;Introns: 16/1

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;34-117/Domain: immunoglobulin homology <IMM>

Query Match 79.7%; Score 573; DB 2; Length 138;
 Best Local Similarity 80.4%; Pred. No. 1.4e-42;
 Matches 111; Conservative 8; Mismatches 19; Indels 0; Gaps 0;

 Qy 1 MNFGLSLIFLVLVLKGVQCEVKLVESGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60
 |||||:|||||:|||||:|||||:|||||:|||||:|||||
 Db 1 MNFGLSLIFLVLILKGVQCEVILVESGGLVKPGGSLKLSCAASGFTFSSYTMSWVRQTP 60

 Qy 61 DKRLEWVASIRSGGGRTYYSDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYCVRYDH 120
 :|||||:| |||| | :|||||:|||||:|||||:|||||:|||||
 Db 61 EKRLEWVATISSLGGNTYPDSVKGRFTISRDNAKNNLYLQMSSLRSEDTALYYCARYYR 120

 Qy 121 YSGSSDYWGQQGTTVTVSS 138
 | ||||| :|||:
 Db 121 YEAWFASWGQGTLVTVSA 138

RESULT 2

B26471

Ig heavy chain precursor V region (MAK33) - mouse
 C;Species: Mus musculus (house mouse)
 C;Date: 05-Jun-1988 #sequence_revision 05-Jun-1988 #text_change 23-Jul-1999
 C;Accession: B26471; S70410
 R;Buckel, P.; Hubner-Parajsz, C.; Mattes, R.; Lenz, H.; Haug, H.; Beaucamp, K.
 Gene 51, 13-19, 1987
 A;Title: Cloning and nucleotide sequence of heavy- and light-chain cDNAs from a
 creatine-kinase-specific monoclonal antibody.
 A;Reference number: A91572; MUID:87248058; PMID:3110009
 A;Accession: B26471
 A;Molecule type: mRNA
 A;Residues: 1-152 <BUC>
 A;Cross-references: GB:M16163; NID:g195405; PIDN:AAA38292.1; PID:g195406
 R;Lebecque, S.G.; Gearhart, P.J.
 J. Exp. Med. 172, 1717-1727, 1990
 A;Title: Boundaries of somatic mutation in rearranged immunoglobulin genes: 5'
 boundary is near the promoter, and 3' boundary is about 1 kb from V(D)J gene.
 A;Reference number: S70410; MUID:91079775; PMID:2258702
 A;Accession: S70410
 A;Status: translation not shown
 A;Molecule type: DNA
 A;Residues: 1-19 <LEB>
 A;Cross-references: EMBL:X53776; NID:g52475; PIDN:CAA37792.1; PID:g52476
 C;Genetics:
 A;Introns: 16/1
 C;Superfamily: immunoglobulin V region; immunoglobulin homology
 C;Keywords: heterotetramer; immunoglobulin
 F;1-19/Domain: signal sequence #status predicted <SIG>
 F;20-152/Product: Ig heavy chain V region MAK33 #status predicted <MAT>
 F;34-117/Domain: immunoglobulin homology <IMM>

Query Match 79.1%; Score 569; DB 2; Length 152;
 Best Local Similarity 78.2%; Pred. No. 3.5e-42;
 Matches 111; Conservative 10; Mismatches 17; Indels 4; Gaps 1;

 Qy 1 MNFGLSLIFLVLVLKGVQCEVKLVESGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60
 |||||:|||||:|||||:|||||:|||||:|||||:|||||

Db 1 MNFGLSLIFLVLVLKGVQCEVQGVESGGLVKPGGSLKLSCHAASGFTFSYDYYMYWVRQTP 60
 Qy 61 DKRLEWVASIRSGGGRTYYSDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYCVR--- 117
 :|||||:||| :|||||:|||||:|||||:|||||:|||||:|||||
 Db 61 EKRLEWVATISDGGSYTYYPDSVKGRFTISRDNAKNLYLQMSSLKSEDTAMYYCARDKA 120
 Qy 118 -YDHYSGSSDYWGQGTTVTVSS 138
 | :| :|||||:|||||
 Db 121 YYGNYGDAMDYWGQGTSVTVSS 142

RESULT 3

S38808

Ig heavy chain - mouse

C;Species: Mus musculus (house mouse)
 C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 21-Jan-2000
 C;Accession: S38808

R;Sequeira, A.; Avrameas, S.; Jouvin-Marche, E.

Immunogenetics 36, 15-21, 1992

A;Title: Molecular characterization of the variable regions of a mouse polyreactive IgG2b antibody with rheumatoid factor activity.

A;Reference number: S38807; MUID:92267566; PMID:1587549

A;Accession: S38808

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-139 <SEQ>

A;Cross-references: EMBL:X53400

A;Note: the authors translated the codon GAG for residue 117 as Lys

A;Note: the sequence of residues 134-139 and the corresponding nucleotide sequence are not shown in this paper

C;Superfamily: immunoglobulin V region; immunoglobulin homology

F;34-116/Domain: immunoglobulin homology <IMM>

Query Match 77.8%; Score 559.5; DB 2; Length 139;
 Best Local Similarity 79.3%; Pred. No. 2.1e-41;
 Matches 111; Conservative 8; Mismatches 16; Indels 5; Gaps 2;

Qy 1 MNFGLSLIFLVLVLKGVQCEVKLVESGGLVKPGASLKLSCHAASGFTFSNYGMSWVRQNS 60
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 Db 1 MNFGFSLIFLVLVLKGVQCEVKLVESGGLVKPGGSLKLSCHAASGFTFSSYAMSWVRQTP 60
 Qy 61 DKRLEWVASIRSGGGRTYYSDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYCVRDH 120
 :|||||:||| :|||||:|||||:|||||:|||||:|||||
 Db 61 EKRLEWVASI-SRGGTTYYPDSVKGRFTISRDNARNLYLQMSSLRSEDTAMYYCAREGI 119
 Qy 121 YSG----SSDYWGQGTTVTV 136
 | | :|||||:|||
 Db 120 YYGYALYGMWDYWGQGTSVTV 139

RESULT 4

C34903

Ig heavy chain precursor V region (5-27) - mouse

C;Species: Mus musculus (house mouse)

C;Date: 27-Jul-1990 #sequence_revision 27-Jul-1990 #text_change 16-Aug-1996

C;Accession: C34903

R;Bedzyk, W.D.; Herron, J.N.; Edmundson, A.B.; Voss Jr., E.W.

Db 61 GKGLEWVAFIRYDGNSKYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAR-DH 119
Qy 121 YSGSS--DYWGQQGTTVTVSS 138
| :: ||||| | |||||
Db 120 IVGATYFDYWGQGTLVTVSS 139

RESULT 6
S31686
Ig heavy chain V region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: S31686
R;Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
submitted to the EMBL Data Library, June 1992
A;Description: Mechanisms that generate human immunoglobulin diversity operate
from the 8th week of gestation in feral liver.
A;Reference number: S31585
A;Accession: S31686
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-140 <CUI>
A;Cross-references: EMBL:Z14205; NID:g30969; PIDN:CAA78574.1; PID:g30970
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;34-117/Domain: immunoglobulin homology <IMM>

Query Match 71.9%; Score 517; DB 2; Length 140;
Best Local Similarity 70.7%; Pred. No. 9.9e-38;
Matches 99; Conservative 17; Mismatches 22; Indels 2; Gaps 1;

Qy 1 MNFGLSLIFLVVLVKGVQCEVKLVESGGGLVKPGASLKSCAASGFTFSNYGMSWVRQNS 60
| |||| : || :||||||| : :||||||| : || || :||||||| : || |||||
Db 1 MEFGLSWLSLVAILKGVQCEVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAP 60

Qy 61 DKRLEWVASIRSGGGRTYYSDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYCVRYDH 120
| |||| : | || |||| : ||||||| : : || ||||| : || : ||||| : ||| :
Db 61 GKGLEWVSAISGSGGSTYYSDSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKCPF 120

Qy 121 YSGSS--DYWGQQGTTVTVSS 138
| | ||||| | |||||
Db 121 AGGSPSPFDYWGQGTLVTVSS 140

RESULT 7
S05271
Ig heavy chain precursor - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 16-Aug-1996
C;Accession: S05271; S04602
R;Kishimoto, T.
submitted to the EMBL Data Library, March 1989
A;Reference number: S05270
A;Accession: S05271
A;Molecule type: mRNA
A;Residues: 1-160 <KIS1>
A;Cross-references: EMBL:X14584

R; Kishimoto, T.; Okajima, H.; Okumoto, T.; Taniguchi, M.

Nucleic Acids Res. 17, 4385, 1989

A; Title: Nucleotide sequences of the cDNAs encoding the V-regions of H- and L-chains of a human monoclonal antibody with broad reactivity to malignant tumor cells.

A; Reference number: S04601; MUID:89296497; PMID:2500644

A; Accession: S04602

A; Molecule type: mRNA

A; Residues: 1-144 <KIS2>

A; Cross-references: EMBL:X14584

C; Superfamily: immunoglobulin V region; immunoglobulin homology

C; Keywords: heterotetramer; immunoglobulin

F; 1-19/Domain: signal sequence #status predicted <SIG>

F; 20-160/Product: Ig heavy chain (fragment) #status predicted <MAT>

F; 34-117/Domain: immunoglobulin homology <IMM>

Query Match 71.8%; Score 516; DB 2; Length 160;
Best Local Similarity 68.1%; Pred. No. 1.4e-37;
Matches 98; Conservative 18; Mismatches 22; Indels 6; Gaps 1;

Qy 1 MNFGLSLIFLVVLKGVCVKLVESGGLVKGASLKLSAASGFTFSNYGMSWVRQNS 60
| |||| :||| :|||||||:|:|||||||:||| :||||||| | |||||

Db 1 MEFGLSWLFLVAILKGVCVKLVEQLLESGGGLVQPGGSLRLSCAASGFTFSTYAMSWVRQAP 60

Qy 61 DKRLEWVASIRSGGGRTYYSDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYCVR--- 117
| ||||:| | | | :|:|||||||:|:|||||||:|:|:|:|:|:|:| :

Db 61 GKGLEWVSAISGSGGSTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKAVV 120

Qy 118 ---YDHYSGSSDYWGQGTTVTVSS 138
:| | | | | | | | | | |

Db 121 RGVISYYYYGMDVWGQGTTVTVSS 144

RESULT 3

S31699

Ig heavy chain V region - human (fragment)

C; Species: Homo sapiens (man)

C; Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999

C; Accession: S31699

R; Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.

submitted to the EMBL Data Library, June 1992

A; Description: Mechanisms that generate human immunoglobulin diversity operate from the 8th week of gestation in feral liver.

A; Reference number: S31585

A; Accession: S31699

A; Status: preliminary

A; Molecule type: mRNA

A; Residues: 1-134 <CUI>

A; Cross-references: EMBL:Z14201; NID:g30961; PIDN:CAA78570.1; PID:g30962

C; Superfamily: immunoglobulin V region; immunoglobulin homology

C; Keywords: heterotetramer; immunoglobulin

F; 34-117/Domain: immunoglobulin homology <IMM>

Query Match 71.5%; Score 514; DB 2; Length 134;
Best Local Similarity 71.0%; Pred. No. 1.7e-37;
Matches 98; Conservative 16; Mismatches 20; Indels 4; Gaps 1;

```

QY      1 MNFGLSLIFLVLVLKGVQCEVKLVESGGGLVKPGASLKLSCHAASGFTFSNYGMSWVRQNS 60
       | |||| :||| :|||||||:|:||||||| || ||:|||||||:| |||||
Db      1 MEFGLSWLFLVAILKGVQCEVQLLESGGGLVHPGGSLRLSCAASGFTFSSYAMSWVRQAP 60

QY      61 DKRLEWVASIRSGGGRTYYSDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYCVRYDH 120
       | ||||:| || |||:| ||| |||:|:| ||| |||:|:| |||:| ||| |
Db      61 GKGLEWVSAISGSGGSTYYSDSVKGRLTISRDN SKNTLYLQMNSLRAEDTAVYYCARW-- 118

QY      121 YSGSSDYWGQGTTVTVSS 138
       ||||||| |||||
Db      119 --RDLDYWGQGTLVTVSS 134

```

RESULT 9

S31588

Ig heavy chain V region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: S31588
R;Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
submitted to the EMBL Data Library, June 1992
A;Description: Mechanisms that generate human immunoglobulin diversity operate
from the 8th week of gestation in feral liver.
A;Reference number: S31585
A;Accession: S31588
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-140 <CUI>
A;Cross-references: EMBL:Z14200; NID:g30957; PIDN:CAA78569.1; PID:g30958
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;34-117/Domain: immunoglobulin homology <IMM>

Query Match 71.3%; Score 513; DB 2; Length 140;
Best Local Similarity 69.3%; Pred. No. 2.2e-37;
Matches 97; Conservative 20; Mismatches 21; Indels 2; Gaps 1;

```

QY      1 MNFGLSLIFLVLVLKGVQCEVKLVESGGGLVKPGASLKLSCHAASGFTFSNYGMSWVRQNS 60
       | |||| :||| :|||||||:|:||||||| || ||:|||||||:| |||||
Db      1 MEFGLSWLFLVAILRGVQCEVQLLESGGGLVQP GGSLRLSCAASGFTFSSYAMSWVRQAP 60

QY      61 DKRLEWVASIRSGGGRTYYSDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYCVRYDH 120
       | ||||:| || |||:| ||| |||:|:| ||| |||:|:| |||:| ||| |
Db      61 GKGLEWVSAISGSGGSTYYADSVKGRFTISRDDS KNTLYLQMNSLRAEDTAVYYCAKDHD 120

QY      121 YSG--SSDYWGQGTTVTVSS 138
       || ||||||| |||||
Db      121 YSNYIYFDYWGQGTLVTVSS 140

```

RESULT 10

HVMS84

Ig heavy chain precursor V region (5-84) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 31-Mar-1997
C;Accession: JT0505
R;Levy, N.S.; Malipiero, U.V.; Lebecque, S.G.; Gearhart, P.J.

J. Exp. Med. 169, 2007-2019, 1989

A;Title: Early onset of somatic mutation in immunoglobulin VH genes during the primary immune response.
A;Reference number: JT0501; MUID:89279149; PMID:2499654
A;Accession: JT0505
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-117 <LEV>
A;Experimental source: strain BALB/cJ
A;Note: this sequence belongs to the VH7183 subfamily
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-117/Product: Ig heavy chain V region (5-84) #status predicted <MAT>
F;34-117/Domain: immunoglobulin homology <IMM>
F;41-115/Disulfide bonds: #status predicted

Query Match 71.2%; Score 512; DB 1; Length 117;
Best Local Similarity 84.6%; Pred. No. 2.2e-37;
Matches 99; Conservative 6; Mismatches 12; Indels 0; Gaps 0;

Qy 1 MNFGLSLIFLVVLKGVLCEVKLVESGGGLVKGASLKLSCAASGFTFSNYGMSWVRQNS 60
 ||||||||| ||||| ||||| | :| ||| ||| ||| :| ||| ||| ||| :| ||| |||
Db 1 MNFGLSLIFLVVLKGVLCEVKLVESGGGLVQPGGSLKLSCAASGFTFSSYTMSWVRQTP 60

Qy 61 DKRLEWVASIRSGGGRTYYSDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYCVR 117
 :| ||| ||| :| :| ||| | ||| ||| :| ||| ||| ||| :| ||| |||
Db 61 EKRLÉWVAYISNGGGSTYYPTVKGRFTISRDNAKNNLYLQMSSLKSEDTAMYYCAR 117

RESULT 11

HVMS34

Ig heavy chain precursor V region (345) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 31-Mar-1997
C;Accession: JT0502
R;Levy, N.S.; Malipiero, U.V.; Lebecque, S.G.; Gearhart, P.J.
J. Exp. Med. 169, 2007-2019, 1989
A;Title: Early onset of somatic mutation in immunoglobulin VH genes during the primary immune response.
A;Reference number: JT0501; MUID:89279149; PMID:2499654
A;Accession: JT0502
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-117 <LEV>
A;Experimental source: strain BALB/cJ
A;Note: this sequence belongs to the VH7183 subfamily
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-117/Product: Ig heavy chain V region (345) #status predicted <MAT>
F;34-117/Domain: immunoglobulin homology <IMM>
F;41-115/Disulfide bonds: #status predicted

Query Match 70.9%; Score 510; DB 1; Length 117;
Best Local Similarity 83.8%; Pred. No. 3.3e-37;
Matches 98; Conservative 6; Mismatches 13; Indels 0; Gaps 0;

A;Accession: S22657
A;Molecule type: mRNA
A;Residues: 1-140 <HIR>
A;Cross-references: EMBL:X59134
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-140/Product: Ig heavy chain (fragment) #status predicted <MAT>
F;34-117/Domain: immunoglobulin homology <IMM>

Query Match 70.1%; Score 504; DB 2; Length 140;
Best Local Similarity 68.1%; Pred. No. 1.3e-36;
Matches 94; Conservative 21; Mismatches 19; Indels 4; Gaps 1;

Qy 1 MNFGLSLIFLVVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60
| |||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 1 MEFGLSWVFLVAILEGVQCEVQLVESGGLVQPGGSLRLSCAASGFTFSSHWMTWVRQTP 60

Qy 61 DKRLEWVASIRSGGGRTYYSDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYCVRYDH 120
||||| :|: | ||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 61 GKRLEWVANVKQDGSAARYYADSVRGRFTISRDNAKNSLYLQMDSLRAADDTAVYYCAR-- 117

Qy 121 YSGSSDYWGQGTTVTVSS 138
| ||||| |||||
Db 118 -STGIDYWGQGTLVTVSS 134

RESULT 14
G1MS21
Ig heavy chain precursor V region (MOPC 21) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 02-Apr-1982 #sequence_revision 02-Apr-1982 #text_change 22-Jun-1999
C;Accession: E90809; A93184; A02066
R;Bothwell, A.L.M.; Paskind, M.; Reth, M.; Imanishi-Kari, T.; Rajewsky, K.;
Baltimore, D.
Cell 24, 625-637, 1981
A;Title: Heavy chain variable region contribution to the NP(b) family of
antibodies: somatic mutation evident in a gamma2a variable region.
A;Reference number: A90809; MUID:81234548; PMID:6788376
A;Accession: E90809
A;Molecule type: mRNA
A;Residues: 1-136 <BOT>
A;Cross-references: GB:J00522; NID:g195052; PIDN:AAD15290.1; PID:g195055
R;Adetugbo, K.; Milstein, C.; Secher, D.S.
Nature 265, 299-304, 1977
A;Title: Molecular analysis of spontaneous somatic mutants.
A;Reference number: A93184; MUID:77100368; PMID:401950
A;Contents: myeloma protein MOPC 21
A;Accession: A93184
A;Molecule type: protein
A;Residues: 17-74,'D',76-77,'H',79-88,'ND',91-114,'H',116-119,'W',121-136 <ADE>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-16/Domain: signal sequence (fragment) #status predicted <SIG>
F;17-136/Product: Ig heavy chain V region (MOPC 21) #status experimental <MAT>
F;31-114/Domain: immunoglobulin homology <IMM>
F;115-119/Region: D segment

F;120-136/Region: J segment (JH4)

F;38-112/Disulfide bonds: #status experimental

Query Match 69.9%; Score 502.5; DB 1; Length 136;
Best Local Similarity 70.4%; Pred. No. 1.7e-36;
Matches 95; Conservative 20; Mismatches 19; Indels 1; Gaps 1;

Qy 5 LSLIFLVVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNSDKRL 64
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 2 LNLVFLVLILKGVQCDVQLVESGGGLVQPGGSRKLSKAASGFTFSSFGMHWVRQAPEKGL 61

Qy 65 EWVASIRSGGGRTYYSDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYCVRYDHYS-G 123
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 62 EWVAYISSGSSTLHYADTVKGRFTISRDNPKNTLFLQMTSLRSEDTAMYYCARWGNYPYY 121

Qy 124 SSDYWGQGTTVTVSS 138
: | : | : | : | : |
Db 122 AMDYWGQGTSVTVSS 136

RESULT 15

S31666

Ig heavy chain V region - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999

C;Accession: S31666

R;Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
submitted to the EMBL Data Library, June 1992

A;Description: Mechanisms that generate human immunoglobulin diversity operate
from the 8th week of gestation in feral liver.

A;Reference number: S31585

A;Accession: S31666

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-138 <CUI>

A;Cross-references: EMBL:Z14202; NID:g30963; PIDN:CAA78571.1; PID:g30964

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;34-117/Domain: immunoglobulin homology <IMM>

Query Match 69.8%; Score 502; DB 2; Length 138;
Best Local Similarity 67.6%; Pred. No. 1.9e-36;
Matches 96; Conservative 21; Mismatches 17; Indels 8; Gaps 2;

Qy 1 MNFGLSLIFLVVLKGVQCEVKLVESGGGLVKPGASLKLSCAASGFTFSNYGMSWVRQNS 60
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 1 MEFGLSWLFLVAILKGVQCEVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAP 60

Qy 61 DKRLEWVASIRSGGGRTYYSDNVKGRFTISRENAKNTLYLQMSSLKSEDTALYYCVR--- 117
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 61 GKGLEWVSAISGSGGSTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKART 120

Qy 118 -YDHYSGSSDYWGQGTTVTVSS 138
| : | : | : | : | : | : |
Db 121 GYWYF----DLWGRGTLVTVSS 138

Search completed: May 17, 2004, 11:33:09
Job time : 14.8 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 17, 2004, 11:23:58 ; Search time 34.7111 Seconds
(without alignments)
1199.858 Million cell updates/sec

Title: US-10-010-942B-2

Perfect score: 692

Sequence: 1 MMSPAQFLFLVLWIRETNG.....CWQGTHFPRTFGGGTKLEIK 132

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SPTREMBL_25:*

1: sp_archea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_mhc:*

8: sp_organelle:*

9: sp_phage:*

10: sp_plant:*

11: sp_rat:*

12: sp_virus:*

13: sp_vertebrate:*

14: sp_unclassified:*

15: sp_rvirus:*

16: sp_bacteriap:*

17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query					Description
No.	Score	Match	Length	DB	ID	

1	611	88.3	148	11	Q8K122	Q8k122 mus musculu
2	583	84.2	239	11	Q8K0F8	Q8k0f8 mus musculu
3	511	73.8	239	4	Q8TCDO	Q8tcd0 homo sapien
4	471	68.1	239	4	Q8NEK0	Q8nek0 homo sapien
5	460	66.5	238	11	Q99M37	Q99m37 mus musculu
6	459	66.3	238	11	Q8VC16	Q8vci6 mus musculu
7	453	65.5	239	11	Q8VC55	Q8vc55 mus musculu
8	444.5	64.2	114	4	Q9UL80	Q9ul80 homo sapien
9	398	57.5	104	11	Q9JL82	Q9jl82 mus musculu
10	362.5	52.4	236	11	Q7TS98	Q7ts98 mus musculu
11	348.5	50.4	111	11	Q811U6	Q811u6 mus musculu
12	346	50.0	86	4	Q7Z3Y5	Q7z3y5 homo sapien
13	341.5	49.3	111	11	Q920E9	Q920e9 mus musculu
14	329.5	47.6	234	11	Q8R062	Q8r062 mus musculu
15	323.5	46.7	234	11	Q91WF8	Q91wf8 mus musculu
16	322.5	46.6	234	4	Q7Z473	Q7z473 homo sapien
17	322	46.5	109	4	Q9UL78	Q9ul78 homo sapien
18	321.5	46.5	236	11	Q7TMK3	Q7tmk3 mus musculu
19	315.5	45.6	107	11	Q9ERZ9	Q9erz9 mus musculu
20	313.5	45.3	134	11	Q8VDD0	Q8vdd0 mus musculu
21	313.5	45.3	237	13	Q7SZ36	Q7sz36 xenopus lae
22	311	44.9	107	4	Q96SA9	Q96sa9 homo sapien
23	307.5	44.4	108	11	Q8VIJ0	Q8vij0 mus musculu
24	307.5	44.4	236	4	Q7Z3Y4	Q7z3y4 homo sapien
25	306.5	44.3	214	11	Q9R1A5	Q9rla5 mus musculu
26	305.5	44.1	108	4	Q9UL70	Q9ul70 homo sapien
27	304.5	44.0	108	4	Q9UL79	Q9ul79 homo sapien
28	303.5	43.9	127	11	Q925S9	Q925s9 mus musculu
29	301.5	43.6	108	4	Q9UL77	Q9ul77 homo sapien
30	298.5	43.1	233	11	Q91WS9	Q91ws9 mus musculu
31	296	42.8	112	11	Q8K1F2	Q8k1f2 mus musculu
32	295	42.6	107	4	Q9UL81	Q9ul81 homo sapien
33	295	42.6	114	11	Q8K1F1	Q8k1f1 mus musculu
34	294	42.5	112	11	Q8K1F3	Q8k1f3 mus musculu
35	293.5	42.4	103	11	Q9JL80	Q9jl80 mus musculu
36	292	42.2	106	5	Q9U410	Q9u410 schistosoma
37	291.5	42.1	108	4	Q9UL83	Q9ul83 homo sapien
38	290	41.9	109	4	Q9UL86	Q9ul86 homo sapien
39	289.5	41.8	235	11	Q91W12	Q91w12 mus musculu
40	288.5	41.7	99	11	Q9JL74	Q9jl74 mus musculu
41	288	41.6	109	4	Q9UL85	Q9ul85 homo sapien
42	288	41.6	131	11	Q811C3	Q811c3 mus musculu
43	287.5	41.5	234	11	Q8VCP0	Q8vcp0 mus musculu
44	280.5	40.5	101	11	Q9JL78	Q9jl78 mus musculu
45	279.5	40.4	235	11	Q7TMK0	Q7tmk0 mus musculu

ALIGNMENTS

RESULT 1

Q8K122

ID Q8K122 PRELIMINARY; PRT; 148 AA.
AC Q8K122;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Salivary gland;
RA Strausberg R.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
DR EMBL; BC028925; AAH28925.1; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00409; IG; 1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Hypothetical protein.
SQ SEQUENCE 148 AA; 16345 MW; 183920BBD9F3B521 CRC64;

Query Match 88.3%; Score 611; DB 11; Length 148;
Best Local Similarity 97.5%; Pred. No. 9.9e-59;
Matches 116; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy	2	MSPAQFLFLLVLWIRETNGYVVMTQTPLTLSVTIGQPASISCKSSQSLLSDGKTYLNWL	61
Db	1	MSPAQFLFLLVLWIRETNGDVVMTQTPLTLSVTIGQPASISCKSSQSLLSDGKTYLNWL	60
Qy	62	LQRPGQSPKRЛИYLVSKLDGVPDRFTGSGSGTDFTLKISRVEAEDLGLYYCWQGTHFP	120
		: : : :	
Db	61	LQRPGQSPKRЛИYLVSKLDGVPDRFTGSGSGTDFTLKISRVEAEDLGVYYCWQGTHFP	119

RESULT 2

Q8K0F8
ID Q8K0F8 PRELIMINARY; PRT; 239 AA.
AC Q8K0F8;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Breast tumor;
RA Strausberg R.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
DR EMBL; BC031498; AAH31498.1; -.
DR PIR; A33933; A33933.
DR PDB; 1KN2; 13-MAR-02.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR002198; ADH_short.

DR InterPro; IPR003599; Ig.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003597; Ig_cl.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; ig; 2.
 DR SMART; SM00409; IG; 2.
 DR SMART; SM00407; IGcl; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS00061; ADH_SHORT; 1.
 DR PROSITE; PS50835; IG_LIKE; 2.
 DR PROSITE; PS00290; IG_MHC; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 239 AA; 26366 MW; D7BE84398AA341F0 CRC64;

Query Match 84.2%; Score 583; DB 11; Length 239;
 Best Local Similarity 87.1%; Pred. No. 2.2e-55;
 Matches 115; Conservative 7; Mismatches 10; Indels 0; Gaps 0;

```

Qy      1 MMSPAQFLFLLVLWIRETNGYVVMQTPLTLSVTIGQPASISCKSSQSLLSDGKTYLNW 60
       ||||||| ||||| :|: | || ||||||| ||| ||| ||| ||| ||| ||| ||| ::|| |::|
Db      1 MMSPAQFLFLLVLSIQEINGDVVMTQTPLTLSVTIGQPASISCKSSQSIFYTNGKMYLSW 60

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Qy      61 LLQRPGQSPKRЛИYLVSKLDGVPDRFTGSGSGTDFTLKISRVEAEDLGLYYCWQGTHFP 120
       ||||||| ||||| :|: | || ||||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |
Db      61 LLQRPGQSPKRЛИLVSКLDGVPDRFSGSGSGTDFTLKISRVEAEDLGVYYCLQSTHFP 120

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Qy      121 RTFGGGTKLEIK 132
       ||||||| |||||
Db      121 YTFGGGTKLEIK 132
  
```

RESULT 3

Q8TCDO

ID Q8TCDO PRELIMINARY; PRT; 239 AA.
 AC Q8TCDO;
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Hypothetical protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lung;
 RA Strausberg R.;
 RL Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; BC022362; AAH22362.1; -.
 DR PIR; S34095; S34095.
 DR PIR; S42267; S42267.
 DR PIR; S42268; S42268.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; ig; 2.

DR SMART; SM00406; IGv; 1.
 DR PROSITE; PS50835; IG_LIKE; 2.
 DR PROSITE; PS00290; IG_MHC; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 239 AA; 26234 MW; FACEDC3A3B03871D CRC64;

 Query Match 73.8%; Score 511; DB 4; Length 239;
 Best Local Similarity 72.7%; Pred. No. 1.6e-47;
 Matches 96; Conservative 18; Mismatches 18; Indels 0; Gaps 0;

 Qy 1 MMSPAQFLFLLVLWIRETNGYVVMQTPLTLSVTIGQPASISCKSSQSLLSDGKTYLNW 60
 | ||| | ||::||: ::| |||||:||:| ||:|||||||:||:||:| ||| |||||
 Db 1 MRLPAQLLGLLMLWPGSSGDVVMTQSPLSLPVTLGQPASISCRSTQSLVYSDGNTYLNW 60

 Qy 61 LLQRPGQSPKRLIYLVSKLDGVPDRFTGSGSGTDFTLKRISRIEAEDLGLYYCWQGTHFP 120
 |||||||:|||| || |||||||:|||||||||:||:||||:||:||:| ||||:
 Db 61 FQQRPGQSPRRLIYKVSNRDGSVPDRFSGSGSGTDFTLKRIVEAEDVGVYFCMCGTHWP 120

 Qy 121 RTFGGGTKLEIK 132
 ||| |||||||
 Db 121 STFGQGTKLEIK 132

RESULT 4

Q8NEKO

ID Q8NEKO PRELIMINARY; PRT; 239 AA.
 AC Q8NEKO;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Hypothetical protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Prostate;
 RA Strausberg R.;
 RL Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; BC030814; AAH30814.1; -.
 DR PIR; S23638; S23638.
 DR PIR; S34091; S34091.
 DR PIR; S40357; S40357.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003597; Ig_cl.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; ig; 2.
 DR SMART; SM00407; IGcl; 1.
 DR SMART; SM00406; IGv; 1.
 DR PROSITE; PS50835; IG_LIKE; 2.
 DR PROSITE; PS00290; IG_MHC; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 239 AA; 26024 MW; F5E20AD3B0552C0A CRC64;

Query Match 68.1%; Score 471; DB 4; Length 239;

Best Local Similarity 68.2%; Pred. No. 3.8e-43;
Matches 90; Conservative 19; Mismatches 23; Indels 0; Gaps 0;

Qy 1 MMSPAQFLFLLVLWIRETNGYVVMTQTPLTLSVTIGQPASISCKSSQSLLSDGKTYLNW 60
| ||| | ||:||: ::| :||||:||:| || |:|||||:||||| ||| ||| :||:
Db 1 MRLPAQLLGLMLWVGSSGDIVMTQSPLSLPVTPEPASISCRSSQSLHSDGNYLDW 60

Qy 61 LLQRPGQSPKRLIYLVSKLDGVPDRFTGSGSGTDFTLKISRERAEIDLGLYYCWQGTHFP 120
||:|||||: |||| | |||||||:|||||||:|||||:||:||| || |
Db 61 YLQKPGQSPQLIYLGSNRASGVDRFSGSGSGTDFTLKISKVEADVGIYYCMQGLQTP 120

Qy 121 RTFGGGTKLEIK 132
:||| |||:|||
Db 121 QTFGQGTKVEIK 132

RESULT 5

Q99M37

ID Q99M37 PRELIMINARY; PRT; 238 AA.
AC Q99M37;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL; BC002035; AAH02035.1; -.
DR PIR; A31807; A31807.
DR PIR; A32248; A32248.
DR PIR; B32248; B32248.
DR PIR; C32248; C32248.
DR PIR; F32530; F32530.
DR PIR; PH1042; PH1042.
DR PIR; PH1043; PH1043.
DR PIR; PH1044; PH1044.
DR PIR; S07455; S07455.
DR PIR; S16112; S16112.
DR PIR; S24500; S24500.
DR PIR; S24501; S24501.
DR PIR; S24503; S24503.
DR PIR; S24504; S24504.
DR PIR; S24529; S24529.
DR PIR; S24532; S24532.
DR PIR; S24533; S24533.
DR PIR; S24535; S24535.
DR PIR; S24536; S24536.
DR PIR; S24538; S24538.
DR PDB; 1I9I; 25-DEC-02.
DR PDB; 1L02; 31-JUL-02.
DR PDB; 1L04; 31-JUL-02.
DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; ig; 2.
 DR SMART; SM00406; IGv; 1.
 DR PROSITE; PS50835; IG_LIKE; 2.
 DR PROSITE; PS00290; IG_MHC; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 238 AA; 26344 MW; FB2B06A0B801330A CRC64;

 Query Match 66.5%; Score 460; DB 11; Length 238;
 Best Local Similarity 69.6%; Pred. No. 6e-42;
 Matches 87; Conservative 17; Mismatches 21; Indels 0; Gaps 0;

 Qy 8 LFLLVLWIRETNGYVVMQTPLTLSVTIGQPASISCKSSQSLLSDGKTYLNWLLQRPGQ 67
 | :|: || :: ||||||||:| |::| |||||:||||:|:| ||| | ||:|||
 Db 7 LLVLMFWIPASSSDVVMTQTPSLPVS LGDQASISCRSSQSIVHSNGNTYLEWYLQKPGQ 66

 Qy 68 SPKRLIYLVSKLDGVPDRFTGSGSGTDFTLKISRREAEDLGLYYC WQGTHFPRTFGGGT 127
 ||| ||| || |||||||:||||| |||||:|||||:||||:|||:| ||| |||
 Db 67 SPKLLIYKVSNRFSGVPDRFSGSGSGTDFTLKISRVEAEDLGVYYCFQGSHVPYTFGSGT 126

 Qy 128 KLEIK 132
 |||||
 Db 127 KLEIK 131

RESULT 6
 Q8VCI6
 ID Q8VCI6 PRELIMINARY; PRT; 238 AA.
 AC Q8VCI6;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Hypothetical protein.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Colon;
 RA Strausberg R.;
 RL Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; BC019760; AAH19760.1; -.
 DR PIR; A27887; A27887.
 DR PIR; A32248; A32248.
 DR PIR; A33933; A33933.
 DR PIR; B27887; B27887.
 DR PIR; B30577; B30577.
 DR PIR; B31485; B31485.
 DR PIR; B32248; B32248.
 DR PIR; B41940; B41940.
 DR PIR; C27887; C27887.
 DR PIR; C32248; C32248.
 DR PIR; C34904; C34904.
 DR PIR; D27887; D27887.
 DR PIR; D29380; D29380.

DR PIR; E28833; E28833.
DR PIR; F32530; F32530.
DR PIR; H31485; H31485.
DR PIR; PH0106; PH0106.
DR PIR; PH1030; PH1030.
DR PIR; PH1031; PH1031.
DR PIR; PH1034; PH1034.
DR PIR; PL0257; PL0257.
DR PIR; PT0359; PT0359.
DR PIR; S07455; S07455.
DR PIR; S16112; S16112.
DR PIR; S26334; S26334.
DR PIR; S53750; S53750.
DR PIR; S60066; S60066.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 2.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KW Hypothetical protein.
SQ SEQUENCE 238 AA; 26224 MW; 35EC08E3DE5414AD CRC64;

Query Match 66.3%; Score 459; DB 11; Length 238;
Best Local Similarity 70.4%; Pred. No. 7.7e-42;
Matches 88; Conservative 16; Mismatches 21; Indels 0; Gaps 0;

Qy 8 LFLLVLWIRETNGYVVMQTPLTLSVTIGQPASISCKSSQSLLSDGKTYLNWLLQRPGQ 67
| :|: || :: ||||||||:| |::| |||||:||||:|:| | ||:| ||:|||
Db 7 LLVLMFWIPASSSDVVMTQTPLSLPVSLGDQASISCRSSQSLVHSNGNTYLHWYLQKPGQ 66

Qy 68 SPKRLIYILVSKLDGVPDRFTGSGSGTDFTLKISRERIEAEDLGLYYCWQGTHFPRTFGGGT 127
||| ||| || |||||||:|||||:|||||:|||||:|||:| | ||| | ||| |||
Db 67 SPKLLIYKVSNRFSGVPDRFSGSGSGTDFTLKISRVEAEDLGVYFCSTHVPPTFGGGT 126

Qy 128 KLEIK 132
|||||
Db 127 KLEIK 131

RESULT 7
Q8VC55
ID Q8VC55 PRELIMINARY; PRT; 239 AA.
AC Q8VC55;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Colon;
RA Strausberg R.;

RL Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
DR EMBL; BC021781; AAH21781.1; -.
DR PIR; A33933; A33933.
DR PDB; 1KC5; 24-JUL-02.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0015070; F:toxin activity; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR004214; Conotoxin.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF02950; Conotoxin; 1.
DR Pfam; PF00047; ig; 2.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KW Hypothetical protein.
SQ SEQUENCE 239 AA; 26303 MW; C16119CACAC25C337 CRC64;

Query Match 65.5%; Score 453; DB 11; Length 239;
Best Local Similarity 67.4%; Pred. No. 3.5e-41;
Matches 89; Conservative 16; Mismatches 27; Indels 0; Gaps 0;

Qy 1 MMSPAQFLFLLVLWIRETNGYVVMTQTPLTLSVTIGQPASISCKSSQSLLSDGKTYLNW 60
| | : ||: :: ||:||||||:| ||| ||||||||::||||:||| ||| :|
Db 1 MKLPVLLVVVLLFTSPASSSDVVLTQTPLSLPVNIGDQASISCKSTKSLINSDGFTYLDW 60

Qy 61 LLQRPGQSPKRЛИYLVSKLDGVPDRFTGSGSGTDFTLKISRVEAEDLGLYYCWQGTHFP 120
||:|||||: ||||||| |||||||:|||||||:||||||:||||:| |||
Db 61 YLQKPGQSPQLLIYLVSNRFSGVPDRFSGSGSGTDFTLKISRVEAEDLGVYYCFQSNHLP 120

Qy 121 RTFGGGTKLEIK 132
|||||||
Db 121 YTFGGGTKEIK 132

RESULT 8
Q9UL80
ID Q9UL80 PRELIMINARY; PRT; 114 AA.
AC Q9UL80;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
(Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).

DR EMBL; AF035034; AAD56270.1; -.
 DR PIR; B49002; B49002.
 DR PIR; S23638; S23638.
 DR PIR; S34094; S34094.
 DR PIR; S34095; S34095.
 DR HSSP; P80362; 1WTL.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; ig; 1.
 DR SMART; SM00406; IGv; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 FT NON_TER 1 1
 FT NON_TER 114 114
 SQ SEQUENCE 114 AA; 12775 MW; 070E31E210D1CB01 CRC64;

Query Match 64.2%; Score 444.5; DB 4; Length 114;
 Best Local Similarity 76.8%; Pred. No. 1.1e-40;
 Matches 86; Conservative 12; Mismatches 13; Indels 1; Gaps 1;

Qy 22 VVMTQTPLTLSVTIGQPASISCKSSQSLLSDGKTYLNWLLQRPGQSPKRLIYLVSKLDS 81
 |||||:||:|| ||:||||||:|||| :||| ||||| |||||||:|||| |||| |||||
 Db 2 VVMTQSPSLPVTLRQPASISCRSSQSPVYSDGNTYLNWFQQRPGQSPRRLIYKVSNRDS 61

Qy 82 GVPDRFTGSGSGTDFTLKISRVEAEDLGLYYCWQGTHFPR-TFGGGTKLEIK 132
 ||||||:|||||||:||||:|||:||| ||||:||| |||||:||| |||||:|||
 Db 62 GVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQGTHWPPWTFGQGTTKVEIK 113

RESULT 9

Q9JL82
 ID Q9JL82 PRELIMINARY; PRT; 104 AA.
 AC Q9JL82;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Anti-myosin immunoglobulin light chain variable region
 (Fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/c;
 RX MEDLINE=20448942; PubMed=10992488;
 RA Malkiel S., Liao L., Cunningham M.W., Diamond B.;
 RT "T-Cell-dependent antibody response to the dominant epitope of
 streptococcal polysaccharide, N-acetyl-glucosamine, is cross-reactive
 with cardiac myosin.";
 RL Infect. Immun. 68:5803-5808(2000).
 DR EMBL; AF206024; AAF69322.1; -.
 DR PIR; S26334; S26334.
 DR HSSP; P01607; 1REI.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; ig; 1.
 DR SMART; SM00406; IGv; 1.

DR PROSITE; PS50835; IG_LIKE; 1.
 FT NON_TER 1 1
 FT NON_TER 104 104
 SQ SEQUENCE 104 AA; 11360 MW; 5DA8BBFD5F0AA1AE CRC64;

 Query Match 57.5%; Score 398; DB 11; Length 104;
 Best Local Similarity 73.1%; Pred. No. 1.2e-35;
 Matches 76; Conservative 13; Mismatches 15; Indels 0; Gaps 0;

 Qy 29 LTLSVTIGQPASISCKSSQSLLSDGKTYLNWLLQPGQSPKRLIYLVSKLDGVPDRFT 88
 |:| |::| |||||:||||: ::| |||:|||:||||| ||| ||| :|||||:
 Db 1 LSLPVSLGDQASISCRSSQSLVHTNGNTYLNHWYLQKPGQSPKLLIYKVSNRFSGVPDRFS 60

 Qy 89 GSGSGTDFTLKISRVEAEDLGLYYCWQGTHFPRTFGGGTKLEIK 132
 |||||:|||||:|||||:|||:||| ||| ||| |||:|||||:
 Db 61 GSGSGTDFTLKISRVEAEDLGVYFCSQTTHVPYTFGGGTKEIK 104

 RESULT 10
 Q7TS98
 ID Q7TS98 PRELIMINARY; PRT; 236 AA.
 AC Q7TS98;
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Anti-colorectal carcinoma light chain.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93383497; PubMed=8372513;
 RA Tonge D.W., Hennam J.F., Greene A.R., Lee I.D., Edge M.D.;
 RT "Cloning and characterization of 1116NS19.9 heavy and light chain
 cDNAs and expression of antibody fragments in Escherichia coli.";
 RL Year Immunol. 7:56-62(1993).
 DR EMBL; S65921; AAB28160.1; -.
 SQ SEQUENCE 236 AA; 26454 MW; 2C586EBF5EA10F4C CRC64;

 Query Match 52.4%; Score 362.5; DB 11; Length 236;
 Best Local Similarity 52.3%; Pred. No. 2.7e-31;
 Matches 69; Conservative 25; Mismatches 33; Indels 5; Gaps 1;

 Qy 1 MMSPAQFLFLLVLWIRETNGYVVMTQTPLTSVTIGQPASISCKSSQSLLSDGKTYLNW 60
 | :||||| :|:|| :| |||:| :: ::| :|:||:|| | :||:|
 Db 3 MRTPAQFLGILLWFPGMKCDIKMTQSPSSMYASLGERVTITCKASQ----DINSYLSW 57

 Qy 61 LLQRPGQSPKRLIYLVSKLDGVPDRFTGSGSGTDFTLKISRVEAEDLGLYYCWQGTHFP 120
 |:||:||| ||| ::| ||| |||:||||| |:| ||| |||:||| | |||
 Db 58 FQQKPGKSPKTLIYRANRLVDGVPSRFSGSGQDYSLTISSELEYEDMGIYYCLQYDEFP 117

 Qy 121 RTFGGGTKLEIK 132
 |||||:|||||:
 Db 118 RTFGGGTKLEIK 129

RESULT 11
Q811U6
ID Q811U6 PRELIMINARY; PRT; 111 AA.
AC Q811U6;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Anti-human Fc gamma receptor III 3G8 kappa light chain variable region
(Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RA Bruenke J., Valerius T., Repp R., Fey G.H.;
RL Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AY173024; AAO18226.1; -.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00409; IG; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Receptor.
FT NON_TER 1 1
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 12101 MW; CEDECEE157F2C94A CRC64;

Query Match 50.4%; Score 348.5; DB 11; Length 111;
Best Local Similarity 58.6%; Pred. No. 3.4e-30;
Matches 65; Conservative 19; Mismatches 26; Indels 1; Gaps 1;

Qy 22 VVMTQTPLTLSVTIGQPASISCKSSQSLLSDGKTYLNWLLQRPGQSPKRLIYLVSKLD 81
:::||:| :|:||:|| |:||||:||| :| || ::|| |:||| || ||| | |:|
Db 1 IVLTQSPASLA VSLGQRATISCKASQS-VDFGDSE MNWYQQKPGQPPKLLI YTTSNLES 59

Qy 82 GVPDRFTGSGSGTDFTLKISRIEAEDLGLYYCWQGTHFPRTFGGGT KLEIK 132
|:| ||: ||||||||| | :| || ||| | | |||||||||:
Db 60 GIPARFSASGS GTDFTLNIHPVEEEDTATYYCQQSNEDPYTFGGGT KLELK 110

RESULT 12
Q7Z3Y5
ID Q7Z3Y5 PRELIMINARY; PRT; 86 AA.
AC Q7Z3Y5;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Rearranged VKA17 V gene segment (Fragment).
GN VKA17.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Hodgkin lymphoma;
 RA Tinguely M., Rosenquist R., Sundstroem C., Amini R.M., Kuppers R.,
 RA Hansmann M.L., Brauninger A.;
 RT "Analysis of a clonally related mantle cell and Hodgkin lymphoma
 RT indicates Epstein-Barr virus infection of a Hodgkin/Reed-Sternberg
 RT cell precursor in a germinal center.";
 RL Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AJ564426; CAD92033.1; -.
 FT NON_TER 1 1
 FT NON_TER 86 86
 SQ SEQUENCE 86 AA; 9764 MW; D198FC04FE0C78FD CRC64;

 Query Match 50.0%; Score 346; DB 4; Length 86;
 Best Local Similarity 79.7%; Pred. No. 4.6e-30;
 Matches 63; Conservative 8; Mismatches 8; Indels 0; Gaps 0;

 Qy 42 SCKSSQSLLDSDGKTYLNWLLQRPGQSPKRLIYLVSKLDGVPDRFTGSGSGTDFTLKIS 101
 ||:|||||: ||| ||||| |||||||:|||| ||| |||||||:|||||||||||
 Db 1 SCRSSQSLVYSDGNTYLNWFQQRPGQSPRRLIYKVSNRDGSVPDRFSGSGSGTDFTLKIS 60

 Qy 102 RIEAEDLGLYYCWQGTHFP 120
 |:||||:|:||| ||||:|
 Db 61 RVEAEDVGVYYCMQGTHWP 79

 RESULT 13
 Q920E9
 ID Q920E9 PRELIMINARY; PRT; 111 AA.
 AC Q920E9;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Pterin-mimicking anti-idiotope kappa chain variable region
 DE (Fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Atkin J.D., Iape A., Jennings I.G., Horaitis O., Cotton R.G.H.;
 RT "Definition of the Idiotope of Pterin-Mimicking Antibodies Expressed
 RT in Mammalian Cells.";
 RL Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AF307935; AAL09419.1; -.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; ig; 1.
 DR SMART; SM00406; IGv; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 FT NON_TER 1 1
 FT NON_TER 111 111
 SQ SEQUENCE 111 AA; 12046 MW; 1E46988AA6858526 CRC64;

```

Query Match          49.3%;  Score 341.5;  DB 11;  Length 111;
Best Local Similarity  57.7%;  Pred. No. 2e-29;
Matches   64;  Conservative  20;  Mismatches  26;  Indels    1;  Gaps     1;

Qy      22 VVMTQTPLTLSVTIGQPASISCKSSQSQLSDGKTYLNWLLQRPGQSPKRЛИYLVSKLDS 81
       :|:||:| :||:||::|| |:||||::|:| : :| :||:|| :|:|| || |:|| |:|
Db      2  IVLTQSPASLAVSLGQRATISCRASKS-VSTSGYSYMHWYQQKPGQPPKLLIYLASNLES 60

Qy      82 GVPDRFTGSGSGTDFTLKISRTEAEDLGLYYCWQGTHFPRTFGGGTKLEIK 132
       ||| ||:||||||| ||| | :| ||| ||| | ||||| ||| |
Db      61 GVPARFSGSGSGTDFTLNIHPVEEEDAATYYCQHSRELPYTFGGGTKEIK 111

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RESULT 14

Q8R062
ID Q8R062 PRELIMINARY; PRT; 234 AA.
AC Q8R062;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Colon;
RA Strausberg R.;
RL Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
DR EMBL; BC027418; AAH27418.1; -.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 2.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KW Hypothetical protein.
SQ SEQUENCE 234 AA; 25857 MW; 4EB08C81426AEAB1 CRC64;

```

Query Match           47.6%; Score 329.5; DB 11; Length 234;
Best Local Similarity 52.3%; Pred. No. 1.1e-27;
Matches 69; Conservative 17; Mismatches 41; Indels 5; Gaps 1;

Y      1 MMSPAQFLLLVLWIRETNGYVVMQTPLTLSVTIGQPASISCKSSQSLLSDGKTYLNW 60
| ||| |||| |::| : | : |||| :|| ::| :||| :|| | : |||| |
O      1 MMSSAQFLGLLLLCFQGTRCDIQMTQTTSSLSASLGDRVТИSCSASQGI-----SNYLNW 55

Y      61 LLQRPGQSPKRЛИYLVSKLDGVPDRFTGSGSGTDFTLKISRIEAEDLGLYYCWQGTHFP 120
|::| : | ||| | | |||| |::| ||||| ::| || :| ||: | || | : |||
O      56 YQQKPDGTVKLLIYYTSSLHSGVPSRFSGSGSGTHYSLTISNLEPEDIATYYCQQYSQFP 115

Y      121 RTFGGGTKLEIK 132
| ||| |||||||
O      116 FTFGSGTKLEIK 127

```

RESULT 15

Q91WF8

ID Q91WF8 PRELIMINARY; PRT; 234 AA.
AC Q91WF8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Colon;
RA Strausberg R.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL; BC015292; AAH15292.1; -.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0005840; C:ribosome; IEA.
DR GO; GO:0003735; F:structural constituent of ribosome; IEA.
DR GO; GO:0006412; P:protein biosynthesis; IEA.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR InterPro; IPR001865; Ribosomal_S2.
DR Pfam; PF00047; ig; 2.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; 1.
DR PROSITE; PS00962; RIBOSOMAL_S2_1; 1.
KW Hypothetical protein.
SQ SEQUENCE 234 AA; 25929 MW; B0D0B0E6EB7812D2 CRC64;

Query Match 46.7%; Score 323.5; DB 11; Length 234;
Best Local Similarity 51.5%; Pred. No. 4.9e-27;
Matches 68; Conservative 19; Mismatches 40; Indels 5; Gaps 1;

Qy 1 MMSPAQFLFLLVLWIRETNGYVVMQTPLTLSVTIGQPASISCKSSQSLLSDGKTYLNW 60
||| |||| ||::| :| :||| :|| ::| :|||:|| | ||||
Db 1 MMSSAQFLGLLLLFCQGTRCDIQMTQTTSSLASLGDRVТИSCRASQ----DISNYLNW 55

Qy 61 LLQRPGQSPKRLIYLVSKLDSGVPDFTGSGSGTDFTLKISRIEAEDLGLYYCWQGTHFP 120
|:| :| ||| |::| ||| ||:|||||:| || :| ||: |:| || |
Db 56 YQQKPDGTVKLLIYYTSRLYLGVPSRFSGSGSGTDYSLTISNLEQEDIATYFCQQQNTPP 115

Qy 121 RTFGGGTKLEIK 132
||| |||||:
Db 116 FTFGSGTKLEVK 127

Search completed: May 17, 2004, 11:32:29
Job time : 35.7111 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 17, 2004, 11:11:13 ; Search time 9.77778 Seconds
(without alignments)
702.947 Million cell updates/sec

Title: US-10-010-942B-2

Perfect score: 692

Sequence: 1 MMSPAQFLFLLVLWIRETNG.....CWQGTHFPRTFGGGTKLEIK 132

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%

Result	Query				Description	
No.	Score	Match	Length	DB	ID	Description
1	508	73.4	133	1	KV2F_HUMAN	P06310 homo sapien
2	434	62.7	113	1	KV2G_MOUSE	P01631 mus musculu
3	417	60.3	117	1	KV2E_HUMAN	P06309 homo sapien
4	415	60.0	113	1	KV2D_HUMAN	P01617 homo sapien
5	414.5	59.9	115	1	KV2A_HUMAN	P01614 homo sapien
6	414	59.8	113	1	KV2B_HUMAN	P01615 homo sapien
7	389.5	56.3	112	1	KV2C_HUMAN	P01616 homo sapien
8	388	56.1	113	1	KV2F_MOUSE	P01630 mus musculu
9	386	55.8	129	1	KV3L_HUMAN	P18135 homo sapien
10	380.5	55.0	134	1	KV4C_HUMAN	P06314 homo sapien
11	380	54.9	113	1	KV2E_MOUSE	P03976 mus musculu
12	374	54.0	112	1	KV2D_MOUSE	P01629 mus musculu
13	374	54.0	120	1	KV2B_MOUSE	P01627 mus musculu
14	373.5	54.0	131	1	KV3I_MOUSE	P01661 mus musculu
15	373	53.9	113	1	KV2C_MOUSE	P01628 mus musculu
16	373	53.9	129	1	KV3M_HUMAN	P18136 homo sapien
17	373	53.9	133	1	KV4B_HUMAN	P06313 homo sapien

18	369	53.3	112	1	KV2A_MOUSE	P01626 mus musculu
19	363.5	52.5	108	1	KV1_CANFA	P01618 canis famil
20	358.5	51.8	111	1	KV3L_MOUSE	P01664 mus musculu
21	358.5	51.8	128	1	KV3K_HUMAN	P06311 homo sapien
22	357	51.6	129	1	KV3H_HUMAN	P04207 homo sapien
23	353.5	51.1	111	1	KV3M_MOUSE	P01665 mus musculu
24	353.5	51.1	111	1	KV3O_MOUSE	P01667 mus musculu
25	352.5	50.9	111	1	KV3N_MOUSE	P01666 mus musculu
26	350.5	50.7	128	1	KV5E_MOUSE	P01637 mus musculu
27	348.5	50.4	111	1	KV3Q_MOUSE	P01669 mus musculu
28	348.5	50.4	111	1	KV3R_MOUSE	P01670 mus musculu
29	347	50.1	110	1	KV3P_MOUSE	P01668 mus musculu
30	343.5	49.6	111	1	KV3J_MOUSE	P01662 mus musculu
31	343.5	49.6	114	1	KV4A_HUMAN	P01625 homo sapien
32	339.5	49.1	111	1	KV3H_MOUSE	P01660 mus musculu
33	337.5	48.8	111	1	KV3U_MOUSE	P01673 mus musculu
34	335.5	48.5	111	1	KV3K_MOUSE	P01663 mus musculu
35	335.5	48.5	111	1	KV3T_MOUSE	P01672 mus musculu
36	335.5	48.5	129	1	KV1W_HUMAN	P04431 homo sapien
37	333.5	48.2	111	1	KV3S_MOUSE	P01671 mus musculu
38	333.5	48.2	132	1	KV3F_MOUSE	P01658 mus musculu
39	333.5	48.2	136	1	KV5B_MOUSE	P01634 mus musculu
40	332.5	48.0	115	1	KV3I_HUMAN	P04433 homo sapien
41	328.5	47.5	108	1	KV5P_MOUSE	P01649 mus musculu
42	328.5	47.5	111	1	KV3C_MOUSE	P01656 mus musculu
43	328.5	47.5	121	1	KV40_HUMAN	P06312 homo sapien
44	325.5	47.0	111	1	KV3A_MOUSE	P01654 mus musculu
45	323.5	46.7	149	1	KV5A_MOUSE	P01633 mus musculu

ALIGNMENTS

RESULT 1

KV2F_HUMAN

ID KV2F_HUMAN STANDARD; PRT; 133 AA.

AC P06310;

DT 01-JAN-1988 (Rel. 06, Created)

DT 01-JAN-1988 (Rel. 06, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE Ig kappa chain V-II region RPMI 6410 precursor.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=86041852; PubMed=2997711;

RA Klobbeck H.G., Meindl A., Combriato G., Solomon A., Zachau H.G.;

RT "Human immunoglobulin kappa light chain genes of subgroups II and III.";

RL Nucleic Acids Res. 13:6499-6513(1985).

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DR EMBL; Z00020; CAA77315.1; -.

DR PIR; A01890; K2HURP.

DR HSSP; P80362; 1WTL.

DR GO; GO:0005576; C:extracellular; NAS.

DR GO; GO:0003823; F:antigen binding; NAS.

DR GO; GO:0006955; P:immune response; NAS.

DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003596; Ig_v.

DR Pfam; PF00047; ig; 1.

DR SMART; SM00406; IGv; 1.

DR PROSITE; PS50835; IG_LIKE; 1.

KW Immunoglobulin V region; Signal.

FT SIGNAL 1 20

FT CHAIN 21 133 IG KAPPA CHAIN V-II REGION RPMI 6410.

FT DOMAIN 21 43 FRAMEWORK-1.

FT DOMAIN 44 59 COMPLEMENTARITY-DETERMINING-1.

FT DOMAIN 60 74 FRAMEWORK-2.

FT DOMAIN 75 81 COMPLEMENTARITY-DETERMINING-2.

FT DOMAIN 82 113 FRAMEWORK-3.

FT DOMAIN 114 122 COMPLEMENTARITY-DETERMINING-3.

FT DOMAIN 123 132 FRAMEWORK-4.

FT DISULFID 43 113 BY SIMILARITY.

FT NON_TER 133 133

SQ SEQUENCE 133 AA; 14707 MW; 513CCAF3673009EE CRC64;

Query Match 73.4%; Score 508; DB 1; Length 133;
Best Local Similarity 73.5%; Pred. No. 3.e-43;
Matches 97; Conservative 16; Mismatches 19; Indels 0; Gaps 0;

Qy	1	MMSPAQFLFLVLWIRETNGYVVMTQTPLTLSVTIGQPASISCKSSQSLLSDGKTYLNW	60
	: :		
Db	1	MRLPAQLLGLMLWPGSSGDVVMTQSPLSLPVTLGQPASISCRSSQSLVYSDGNTYLNW	60
Qy	61	LLQRPGQSPKRЛИYLVSKLDGVPDFGSGSGTDFTLKISRERIEADLGLYYCWQGTHFP	120
	: :		
Db	61	FQQRPGQSPRRLIYKVSNRDSGVPDFRGSGSGSGTDFTLKISREREAEDVGVYYCMQGTHWS	120
Qy	121	RTFGGGTKLEIK	132
	:		
Db	121	WTFGOGTKVEIK	132

RESULT 2

KV2G MOUSE

ID KV2G_MOUSE STANDARD; PRT; 113 AA.
AC P01631;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-II region 26-10.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vert
OC Mammalia; Eutheria; Rodentia; Sciurognathi;

OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=A/J;
 RX MEDLINE=83178921; PubMed=6404298;
 RA Novotny J., Margolies M.N.;
 RT "Amino acid sequence of the light chain variable region from a mouse
 anti-digoxin hybridoma antibody.";
 RL Biochemistry 22:1153-1158(1983).
 CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGG2A HYBRIDOMA
 CC PROTEIN THAT BINDS DIGOXIN.
 DR PIR; A01914; KVMS26.
 DR HSSP; P80362; 1WTL.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; ig; 1.
 DR SMART; SM00406; IgV; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 KW Immunoglobulin V region; Monoclonal antibody; Hybridoma.
 FT DOMAIN 1 23 FRAMEWORK-1.
 FT DOMAIN 24 39 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 40 54 FRAMEWORK-2.
 FT DOMAIN 55 61 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 62 93 FRAMEWORK-3.
 FT DOMAIN 94 102 COMPLEMENTARITY-DETERMINING-3.
 FT DOMAIN 103 112 FRAMEWORK-4.
 FT DISULFID 23 93 BY SIMILARITY.
 FT NON_TER 113 113
 SQ SEQUENCE 113 AA; 12273 MW; F9F39CE949A84C2A CRC64;

 Query Match 62.7%; Score 434; DB 1; Length 113;
 Best Local Similarity 75.7%; Pred. No. 5.5e-36;
 Matches 84; Conservative 11; Mismatches 16; Indels 0; Gaps 0;

 Qy 22 VVMTQTPLTLSVTIGQPASISCKSSQSLDSDGKTYLNWLLQRPGQSPKRLIYLVSKLDS 81
 |||||||:| |::| |||||:|||||: |:| ||||| ||: ||||| ||| |||
 Db 2 VVMTQTPLSLPVSLGQASISCRSSQSLVHSNGNTYLNWYLQKAGQSPKLLIYKVSNRFS 61

 Qy 82 GVPDRFTGSGSGTDFTLKISRVEAEDLGLYYCWQGTHFPRTFGGGTKLEIK 132
 ||||||:|||||||:|||||:|||||:|:| | | | ||| |||||
 Db 62 GVPDRFSGSGSGTDFTLKISRVEAEDLGIYFCSQTTVPPTFGGGTKLEIK 112

RESULT 3

KV2E_HUMAN

ID KV2E_HUMAN STANDARD; PRT; 117 AA.
 AC P06309;
 DT 01-JAN-1988 (Rel. 06, Created)
 DT 01-JAN-1988 (Rel. 06, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig kappa chain V-II region GM607 precursor (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.

RX MEDLINE=84191506; PubMed=6325927;
 RA Klobeck H.G., Solomon A., Zachau H.G.;
 RT "Contribution of human V kappa II germ-line genes to light-chain diversity.";
 RL Nature 309:73-76 (1984).
 CC -----
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 CC -----
 DR EMBL; Z00009; -; NOT_ANNOTATED_CDS.
 DR PIR; A01889; K2HUGM.
 DR HSSP; P80362; 1WTL.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; F:antigen binding; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; ig; 1.
 DR SMART; SM00406; IGv; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 KW Immunoglobulin V region; Signal.
 FT NON_TER 1 1
 FT SIGNAL <1 4
 FT CHAIN 5 117 IG KAPPA CHAIN V-II REGION GM607.
 FT DOMAIN 5 27 FRAMEWORK-1.
 FT DOMAIN 28 43 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 44 58 FRAMEWORK-2.
 FT DOMAIN 59 65 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 66 97 FRAMEWORK-3.
 FT DOMAIN 98 106 COMPLEMENTARITY-DETERMINING-3.
 FT DOMAIN 107 116 FRAMEWORK-4.
 FT DISULFID 27 97 BY SIMILARITY.
 FT NON_TER 117 117
 SQ SEQUENCE 117 AA; 12664 MW; 92C57DC719E558B1 CRC64;

 Query Match 60.3%; Score 417; DB 1; Length 117;
 Best Local Similarity 69.6%; Pred. No. 2.7e-34;
 Matches 80; Conservative 17; Mismatches 18; Indels 0; Gaps 0;

 Qy 18 TNGYVVMTQTPLTLSVTIGQPASISCKSSQSLLSDGKTYLNWLLQRPGQSPKRЛИYLVS 77
 ::| :|||:|||:||| || |:|||||:||||| ||:| ||:| ||:| |||:| ||| |
 Db 2 SSGDIVMTQSPLSLPVTPGEPASISCRSSQSLLHSNGNYLDWYLQKPQQSPQLIYLGS 61

 Qy 78 KLDGVPDRFTGSGSGTDFTLKISRVEAEDLGLYYCWQGTHFPRTFGGGTKLEIK 132
 |||||||:|||||:|||:|||:|:||| || |:||| |||:|||:
 Db 62 NRASGVPDRFSGSGSGTDFTLKISRVEAEDGVYYCMQGLQTPQTFGQGKTKEIK 116

RESULT 4
 KV2D_HUMAN
 ID KV2D_HUMAN STANDARD; PRT; 113 AA.
 AC P01617;

DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig kappa chain V-II region TEW.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE (BENCE-JONES PROTEIN TEW).
 RX MEDLINE=74148480; PubMed=4596149;
 RA Putnam F.W., Whitley E.J. Jr., Paul C., Davidson J.N.;
 RT "Amino acid sequence of a kappa Bence Jones protein from a case of
 primary amyloidosis.";
 RL Biochemistry 12:3763-3780 (1973).
 RN [2]
 RP SEQUENCE OF 1-27 (AMYLOID PROTEIN TEW).
 RX MEDLINE=73166638; PubMed=4700495;
 RA Terry W.D., Page D.L., Kimura S., Isobe T., Osseman E.F.,
 RA Glenner G.G.;
 RT "Structural identity of Bence Jones and amyloid fibril proteins in a
 patient with plasma cell dyscrasia and amyloidosis.";
 RL J. Clin. Invest. 52:1276-1281 (1973).
 CC -!- MISCELLANEOUS: THE MAJOR AMYLOID PROTEIN APPEARS TO BE IDENTICAL
 CC WITH THE BENCE JONES PROTEIN ISOLATED FROM THE SAME PATIENT.
 CC -!- MISCELLANEOUS: THIS PROTEIN WAS ISOLATED FROM THE URINE OF A
 CC PATIENT WITH PLASMA CELL DYSCRASIA AND AMYLOIDOSIS.
 CC -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2)
 CC MARKER.
 DR PIR; A90370; K2HUTW.
 DR HSSP; P01607; 1REI.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; F:antigen binding; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; ig; 1.
 DR SMART; SM00406; IGv; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 KW Immunoglobulin V region; Bence-Jones protein; Amyloid.
 FT DOMAIN 1 23 FRAMEWORK-1.
 FT DOMAIN 24 39 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 40 54 FRAMEWORK-2.
 FT DOMAIN 55 61 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 62 93 FRAMEWORK-3.
 FT DOMAIN 94 102 COMPLEMENTARITY-DETERMINING-3.
 FT DOMAIN 103 112 FRAMEWORK-4.
 FT DISULFID 23 93 BY SIMILARITY.
 FT NON_TER 113 113
 SQ SEQUENCE 113 AA; 12316 MW; 0C3C38F81F1843CA CRC64;
 Query Match 60.0%; Score 415; DB 1; Length 113;
 Best Local Similarity 71.2%; Pred. No. 4.1e-34;
 Matches 79; Conservative 14; Mismatches 18; Indels 0; Gaps 0;
 QY 22 VVMTQTPLTLSVTIGQPASISCKSSQSLDSDGKTYLNWLQRPGQSPKRLIYLVSKLD 81
 :||||:||:| || |:|||||:|||||| ||| |||| ||:||||: ||| :| |

Db 2 IVMTQSPLSLPVTPGEPASISCRSSQSLHSDGFDYLNWYLQKPGQSPZLLIYALSNRAS 61
Qy 82 GVPDRFTGSGSGTDFTLKRISRVEAEDLGLYYCWQGTHFPRTFGGGTKLEIK 132
| | | | : | | | | | | | | : | | | : | | | | | | | : | | | : | | |
Db 62 GVPDRFSGSGSGTDFTLKRISRVEAEDVGVYYCMZALQAPITFGQQGTRLEIK 112

RESULT 5

KV2A_HUMAN

ID KV2A_HUMAN STANDARD; PRT; 115 AA.
AC P01614;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-II region Cum.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=68242259; PubMed=5586923;
RA Hilschmann N.;
RT "The complete amino acid sequence of Bence Jones protein Cum (kappa-type).";
RL Hoppe-Seyler's Z. Physiol. Chem. 348:1718-1722(1967).
RN [2]
RP REVISIONS TO 50; 52; 96 AND 97.
RX MEDLINE=70063440; PubMed=4188189;
RA Hilschmann N.;
RT "Molecular basis of antibody formation.";
RL Naturwissenschaften 56:195-205(1969).
CC -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC -!- MISCELLANEOUS: This is a Bence-Jones protein.
DR PIR; B91639; K2HUCM.
DR HSSP; P01607; 1REI.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region; Bence-Jones protein.
FT DISULFID 24 95 BY SIMILARITY.
FT NON_TER 115 115
SQ SEQUENCE 115 AA; 12676 MW; 59E9F90A379569EC CRC64;

Query Match 59.9%; Score 414.5; DB 1; Length 115;
Best Local Similarity 72.3%; Pred. No. 4.7e-34;
Matches 81; Conservative 13; Mismatches 17; Indels 1; Gaps 1;

Qy 22 VVMTQTPLTLSVTIGQPASISCKSSQSLDS-DGKTYLNWLLQRPGQSPKRLIYLVSKLD 80
: | | | | : | | | | : | | | | | | | | | | : | | | : | | | : | | |
Db 3 IVMTQTPLSLPVTPGEPASISCRSSQSLDSDGDGNTYLNWYLQKAGQSPQLLIYTLSYRA 62

Qy	81	SGVPDRFTGSGSGTDFTLKISR <small>EAEIDLGLYYCWQGTHFPRTFGGGTKLEIK</small>	132
		: : : : : : : :	
Db	63	SGVPDRFSGSGSGTDFTLKISR <small>VQAEDVGVYYCMQRLEIPYTFGQG</small> TKLEIR	114

RESULT 6
KV2B_HUMAN
 ID KV2B_HUMAN STANDARD; PRT; 113 AA.
 AC P01615;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig kappa chain V-II region FR.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=76253627; PubMed=821524;
 RA Riesen W.F., Jaton J.-C.;
 RT "Variable region sequence of the light chain from a Waldenstrom's IgM
 with specificity for phosphorylcholine.";
 RL Biochemistry 15:3829-3833 (1976).
 CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A WALDENSTROM'S
 MACROGLOBULIN THAT BINDS PHOSPHORYLCHOLINE.
 DR PIR; A01886; K2HUFR.
 DR HSSP; P01607; IREI.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; F:antigen binding; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; ig; 1.
 DR SMART; SM00406; IGv; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 KW Immunoglobulin V region.
 FT DOMAIN 1 23 FRAMEWORK-1.
 FT DOMAIN 24 39 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 40 54 FRAMEWORK-2.
 FT DOMAIN 55 61 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 62 93 FRAMEWORK-3.
 FT DOMAIN 94 102 COMPLEMENTARITY-DETERMINING-3.
 FT DOMAIN 103 112 FRAMEWORK-4.
 FT DISULFID 23 93 BY SIMILARITY.
 FT NON_TER 113 113
 SQ SEQUENCE 113 AA; 12660 MW; 0C0DA39E46DB96BE CRC64;

 Query Match 59.8%; Score 414; DB 1; Length 113;
 Best Local Similarity 69.4%; Pred. No. 5.1e-34;
 Matches 77; Conservative 16; Mismatches 18; Indels 0; Gaps 0;

 Qy 22 VVMTQTPLTLSVTIGQPASISCKSSQSLLDSDGKTYLNWLLQRPGQSPKRLIYLVSKLDS 81
 |||||:||| | ||:||| | :||||| : : |||:| ||:|||||: ||| | ||| |||
 Db 2 VVMTQSPFLPVTLGEPAQSIQCRSSQSQLVYRBGBTYLBWYLQKPGQSPELLIYLSSYRDS 61

 Qy 82 GVPDRFTGSGSGTDFTLKISRERIAEDLGLYYCWQGTHFPRTFGGGTKLEIK 132

KV2F_MOUSE

ID KV2F_MOUSE STANDARD; PRT; 113 AA.

AC P01630;

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE Ig kappa chain V-II region 7S34.1.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE.

RX MEDLINE=83256427; PubMed=6409088;

RA Chang J.-Y., Herbst H., Aebersold R., Braun D.G.;

RT "A new isotype sequence (V kappa 27) of the variable region of kappa-light chains from a mouse hybridoma-derived anti-(streptococcal group A polysaccharide) antibody containing an additional cysteine residue. Application of the dimethylaminoazobenzene isothiocyanate technique for the isolation of peptides.";

RL Biochem. J. 211:173-180(1983).

CC -!- MISCELLANEOUS: THIS CHAIN IS FROM A HYBRIDOMA-DERIVED MONOCLONAL ANTIBODY AGAINST THE STREPTOCOCCAL GROUP A POLYSACCHARIDE.

DR PIR; A01913; KVMS7S.

DR HSSP; P80362; 1WTL.

DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003596; Ig_v.

DR Pfam; PF00047; ig; 1.

DR SMART; SM00406; IGv; 1.

DR PROSITE; PS50835; IG_LIKE; 1.

KW Immunoglobulin V region; Monoclonal antibody; Hybridoma.

FT DOMAIN 1 23 FRAMEWORK-1.

FT DOMAIN 24 39 COMPLEMENTARITY-DETERMINING-1.

FT DOMAIN 40 54 FRAMEWORK-2.

FT DOMAIN 55 61 COMPLEMENTARITY-DETERMINING-2.

FT DOMAIN 62 93 FRAMEWORK-3.

FT DOMAIN 94 102 COMPLEMENTARITY-DETERMINING-3.

FT DOMAIN 103 112 FRAMEWORK-4.

FT DISULFID 23 93 BY SIMILARITY.

FT NON_TER 113 113

SQ SEQUENCE 113 AA; 12496 MW; 42C019D10ADA3C91 CRC64;

Query Match 56.1%; Score 388; DB 1; Length 113;

Best Local Similarity 67.6%; Pred. No. 1.9e-31;

Matches 75; Conservative 14; Mismatches 22; Indels 0; Gaps 0;

Qy 22 VVMTQTPLTLSVTIGQPASISCKSSQSLLSDGKTYLNWLQRPGQSPKRLIYLVSKLDS 81
 :||||| : || |: ||||:|||:||| ||| | ||||| | : ||| :| |||

Db 2 IVMTQTAPSALVTPGESVSISCRSSKSLLHSNGNTLYWFQRPQCPQLLIYRMSNLAS 61

Qy 82 GVPDRFTGSGSGTDFTLKISRIEAEDLGLYYCWQGTHFPRTFGGGTKLEIK 132
 |||||:||||| |||:|||:|||:||| | :| ||| |||

Db 62 GVPDRFSGSGSGTAFTLRISRVEAEDVGVYYCMQQREYPYTFGGGTKEIK 112

RESULT 9
 KV3L_HUMAN

ID KV3L_HUMAN STANDARD; PRT; 129 AA.
AC P18135;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region HAH precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88171307; PubMed=3127527;
RA Kipps T.J., Tomhave E., Chen P.P., Carson D.A.;
RT "Autoantibody-associated kappa light chain variable region gene
expressed in chronic lymphocytic leukemia with little or no somatic
mutation. Implications for etiology and immunotherapy.";
RL J. Exp. Med. 167:840-852(1988).
CC -!- DISEASE: The protein is one of the surface immunoglobulin M
CC autoantibodies expressed in patients with chronic lymphocytic
CC leukemia.
DR PIR; PL0022; K3HUHA.
DR HSSP; P80362; 1WTL.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 129 IG KAPPA CHAIN V-III REGION HAH.
FT DOMAIN 21 43 FRAMEWORK-1.
FT DOMAIN 44 55 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 56 70 FRAMEWORK-2.
FT DOMAIN 71 77 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 78 109 FRAMEWORK-3.
FT DOMAIN 110 118 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 119 129 JK1 SEGMENT.
FT DISULFID 43 109 BY SIMILARITY.
FT NON_TER 129 129
SQ SEQUENCE 129 AA; 14073 MW; D3C55292772774D0 CRC64;

Query Match 55.8%; Score 386; DB 1; Length 129;
Best Local Similarity 56.8%; Pred. No. 3.4e-31;
Matches 75; Conservative 24; Mismatches 29; Indels 4; Gaps 1;

Qy 1 MMSPAQFLFLVLWIRETNGYVVMTQTPLTLSVTIGQPASISCKSSQSLLSDGKTYLNW 60
| :||| ||||:|||: :|| | :|||:| ||||: | :|||:|||: | | || |
Db 1 METPAQLLFLLLWLPPDTTGEIVLTQSPGTLSLSPGERATLSCRASQSVSSS---YLAW 56

Qy 61 LLQRPGQSPKRЛИYLVSKLDGVPDFTGSGSGTDFTLKISRLEAEDLGLYYCWQGTHFP 120
| :|||:|: ||| | :|||:| |||||:|||:| |||:| || :||| | |
Db 57 YQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGTSP 116

Qy 121 RTFGGGTKLEIK 132
| | | | | : | | |
Db 117 RTFGQGTKVEIK 128

RESULT 10

KV4C_HUMAN

ID KV4C_HUMAN STANDARD; PRT; 134 AA.
AC P06314;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-APR-1988 (Rel. 07, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-IV region B17 precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86041854; PubMed=2997713;
RA Marsh P., Mills F., Gould H.;
RT "Detection of a unique human V kappa IV germline gene by a cloned
RT cDNA probe.";
RL Nucleic Acids Res. 13:6531-6544(1985).
RN [2]
RP REVISION TO 76.
RA Marsh P.;
RL Submitted (OCT-1986) to the EMBL/GenBank/DDBJ databases.
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CC -----
DR EMBL; X02990; CAA26733.1; -.
DR HSSP; P80362; 1WTL.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 134 IG KAPPA CHAIN V-IV REGION B17.
FT DOMAIN 21 43 FRAMEWORK-1.
FT DOMAIN 44 60 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 61 75 FRAMEWORK-2.
FT DOMAIN 76 82 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 83 114 FRAMEWORK-3.
FT DOMAIN 115 121 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 122 133 FRAMEWORK-4.

FT DOMAIN 103 112 FRAMEWORK-4.
 FT DISULFID 23 93 BY SIMILARITY.
 FT NON_TER 113 113
 SQ SEQUENCE 113 AA; 12390 MW; 4E93797046F8DB33 CRC64;

 Query Match 54.9%; Score 380; DB 1; Length 113;
 Best Local Similarity 65.8%; Pred. No. 1.2e-30;
 Matches 73; Conservative 15; Mismatches 23; Indels 0; Gaps 0;

 Qy 22 VVMTQTPLTLSVTIGQPASISCKSSQSLLSDGKTYLNWLLQRPGQSPKRLIYLVSKLDS 81
 :||||| : ||:| |||||:||:||| |:| ||| | |||:|||||: ||| :| |||
 Db 2 IVMTQAVFSNPVTLGTSASISCRSSKSLLHSNGITYLYWYLQKPGQSPQLLYQMSNLAS 61

 Qy 82 GVPDRFTGSGSGTDFTLKISRTEAEDLGLYYCWQGTHFPRTFGGGTKLEIK 132
 |||||||: |||||||:|||:|||:|||:||| ||| |||||||
 Db 62 GVPDRFSSSGSGTDFTLRISRVEAEDVGVYYCAHNLELPYTFGGGTKEIK 112

 RESULT 12
 KV2D_MOUSE
 ID KV2D_MOUSE STANDARD; PRT; 112 AA.
 AC P01629;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig kappa chain V-II region 2S1.3.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=83055101; PubMed=7141411;
 RA Herbst H., Chang J.Y., Aebersold R., Braun D.G.,
 RT "Murine VK25 isotype sequence: monoclonal antibody 2S1.3 specific for
 RT the group A streptococcal polysaccharide.";
 RL Hoppe-Seyler's Z. Physiol. Chem. 363:1069-1076(1982).
 CC -!- MISCELLANEOUS: THIS CHAIN IS FROM A HYBRIDOMA-DERIVED MONOCLONAL
 CC ANTIBODY AGAINST THE STREPTOCOCCAL GROUP A POLYSACCHARIDE.
 DR PIR; A01911; KVMSS1.
 DR HSSP; P01607; 1REI.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; ig; 1.
 DR SMART; SM00406; IGv; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 KW Immunoglobulin V region; Monoclonal antibody.
 FT DOMAIN 1 23 FRAMEWORK-1.
 FT DOMAIN 24 39 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 40 54 FRAMEWORK-2.
 FT DOMAIN 55 61 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 62 93 FRAMEWORK-3.
 FT DOMAIN 94 102 COMPLEMENTARITY-DETERMINING-3.
 FT DOMAIN 103 112 FRAMEWORK-4.
 FT DISULFID 23 93 BY SIMILARITY.
 FT NON_TER 112 112
 SQ SEQUENCE 112 AA; 12221 MW; BD5EF5E6D789FBEC CRC64;

Query Match 54.0%; Score 374; DB 1; Length 112;
 Best Local Similarity 65.8%; Pred. No. 4.5e-30;
 Matches 73; Conservative 13; Mismatches 25; Indels 0; Gaps 0;

 QY 22 VVMTQTPLTLSVTIGQPASISCKSSQSLLSDGKTYLNWLLQRPGQSPKRLIYLVSKLDS 81
 :|||| : ||:| ||||:||:|| | | ||| | ||:||||:||| :||| :| |||
 Db 2 IVMTQAAFSNPVTLGTSASFSCRSSKSLQQSKGITYLYWYLQKPGQSPQLLIYQMSNLAS 61

 QY 82 GVPDRFTGSGSGTDFTLKISRTEAEDLGLYCWQGTHFPRTFGGGTKLEIK 132
 ||||||:|||||:|||:|||:|||:|||:||| |||:|||||:
 Db 62 GVPDRFSGSGSGTDFTLRISRVEAEVGVYYCANLQELPYTFGGGTKEIK 112

RESULT 13

KV2B_MOUSE

ID KV2B_MOUSE STANDARD; PRT; 120 AA.
 AC P01627;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig kappa chain V-II region VKappa167 precursor.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=82002223; PubMed=6791832;
 RA Selsing E., Storb U.;
 RT "Somatic mutation of immunoglobulin light-chain variable-region
 genes.";
 RL Cell 25:47-58 (1981).
 CC -----
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 CC -----
 DR EMBL; J00562; AAA39032.1; -.
 DR EMBL; K02415; AAA39051.1; -.
 DR PIR; A01909; KVMS67.
 DR HSSP; P80362; 1WTL.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; ig; 1.
 DR SMART; SM00406; IGv; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 KW Immunoglobulin V region; Signal.
 FT SIGNAL 1 20
 FT CHAIN 21 120 IG KAPPA CHAIN V-II REGION VKAPPA167.
 FT DOMAIN 21 43 FRAMEWORK-1.
 FT DOMAIN 44 59 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 60 74 FRAMEWORK-2.

FT DOMAIN 75 81 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 82 113 FRAMEWORK-3.
 FT DOMAIN 114 120 COMPLEMENTARITY-DETERMINING-3.
 FT DISULFID 43 113 BY SIMILARITY.
 SQ SEQUENCE 120 AA; 13280 MW; 63BB571F0E4DE3E8 CRC64;

 Query Match 54.0%; Score 374; DB 1; Length 120;
 Best Local Similarity 60.8%; Pred. No. 4.8e-30;
 Matches 73; Conservative 18; Mismatches 29; Indels 0; Gaps 0;

 Qy 1 MMSPAQFLILLVLWIRETNGYVVMQTPLTLSVTIGQPASISCKSSQSLLSDGKTYLNW 60
 | ||| :|| :| :|| :||| | :| ||| :||| :||| |||||
 Db 1 MRCSLQFLGVLMFWISGVSGDIVITQDELSNPVTSGESVSISCRSSKSLLYKDGGKTYLNW 60

 Qy 61 LLQRPGQSPKRЛИYLVSKLDGVPDRFTGSGSGTDFTLKISRIEAEDLGLYYCWQGTHFP 120
 ||||||| : |||| :| ||| ||| :||||| :||| :| :||| | :|
 Db 61 FLQRPGQSPQLLIYLMSTRASGVSDRFSGSGSGTDFTLEISRVKAEDVGVYYCQLVEYP 120

RESULT 14

KV3I_MOUSE

ID KV3I_MOUSE STANDARD; PRT; 131 AA.

AC P01661;

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE Ig kappa chain V-III region MOPC 63 precursor.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE OF 1-35.

RX MEDLINE=78235887; PubMed=98179;

RA Burstein Y., Schechter I.;

RT "Primary structures of N-terminal extra peptide segments linked to the variable and constant regions of immunoglobulin light chain precursors: implications on the organization and controlled expression of immunoglobulin genes.";

RL Biochemistry 17:2392-2400(1978).

RN [2]

RP SEQUENCE OF 21-131.

RX MEDLINE=73140225; PubMed=4691517;

RA McKean D.J., Potter M., Hood L.E.;

RT "Mouse immunoglobulin chains. Pattern of sequence variation among kappa chains with limited sequence differences.";

RL Biochemistry 12:760-771(1973).

RN [3]

RP REVISIONS.

RX MEDLINE=79012520; PubMed=99744;

RA McKean D.J., Bell M., Potter M.;

RT "Mechanisms of antibody diversity: multiple genes encode structurally related mouse kappa variable regions.";

RL Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917(1978).

DR PIR; B90412; KVMSM6.

DR HSSP; P01679; 2FBJ.

DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; ig; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PSS0835; IG_LIKE; 1.
 KW Immunoglobulin V region; Signal.
 FT SIGNAL 1 20
 FT CHAIN 21 131 IG KAPPA CHAIN V-III REGION MOPC 63.
 FT DOMAIN 21 43 FRAMEWORK-1.
 FT DOMAIN 44 58 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 59 73 FRAMEWORK-2.
 FT DOMAIN 74 80 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 81 112 FRAMEWORK-3.
 FT DOMAIN 113 121 COMPLEMENTARITY-DETERMINING-3.
 FT DOMAIN 122 131 FRAMEWORK-4.
 FT DISULFID 43 112 BY SIMILARITY.
 FT NON_TER 131 131
 SQ SEQUENCE 131 AA; 14291 MW; D212EC9F08DC880A CRC64;

 Query Match 54.0%; Score 373.5; DB 1; Length 131;
 Best Local Similarity 53.8%; Pred. No. 6e-30;
 Matches 71; Conservative 27; Mismatches 33; Indels 1; Gaps 1;

 QY 1 MMSPAQFLFLLVLWIRETNGYVVMQTPLTLSVTIGQPASISCKSSQSLLSDGKTYLNW 60
 | : |::|:||: :| :| :||:||:| :|||:||:| :|| | :||:|
 Db 1 METDTLLLWVLLWVPGSTGNIVLTQSPASLAVSLGQRATISCRASES-VDSYGNSFMHW 59

 QY 61 LLQRPGQSPKRЛИYLVSKLDGVPDRFTGSGSGTDFTLKISRIEADLGLYYCWQGTHFP 120
 |:||| ||| | |:||| |||:||| |||:||| |||:||| |||:||| |||:||| |||:|||
 Db 60 YQQKPGQPPKLLIYLASNLESGVPARFSGSGSRTDFTLTIDPVEADDAATYYCQQNNEDP 119

 QY 121 RTFGGGTKLEIK 132
 |||||||||
 Db 120 WTFGGGTKEIK 131

RESULT 15
 KV2C_MOUSE
 ID KV2C_MOUSE STANDARD; PRT; 113 AA.
 AC P01628;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig kappa chain V-II region MOPC 511.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=81052016; PubMed=6776396;
 RA Appella E.;
 RT "Amino acid sequence of the light chain variable region of M511, a phosphorylcholine-binding murine myeloma protein.";
 RL Mol. Immunol. 17:711-718(1980).
 CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT
 CC BINDS PHOSPHORYLCHOLINE.
 DR PIR; A01910; KVMS51.

DR HSSP; P80362; 1WTL.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; ig; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 KW Immunoglobulin V region.
 FT DOMAIN 1 23 FRAMEWORK-1.
 FT DOMAIN 24 39 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 40 54 FRAMEWORK-2.
 FT DOMAIN 55 61 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 62 93 FRAMEWORK-3.
 FT DOMAIN 94 102 COMPLEMENTARITY-DETERMINING-3.
 FT DOMAIN 103 112 FRAMEWORK-4.
 FT DISULFID 23 93 BY SIMILARITY.
 FT NON_TER 113 113
 SQ SEQUENCE 113 AA; 12496 MW; EFB0DC4DA2BD3450 CRC64;

 Query Match 53.9%; Score 373; DB 1; Length 113;
 Best Local Similarity 64.9%; Pred. No. 5.7e-30;
 Matches 72; Conservative 16; Mismatches 23; Indels 0; Gaps 0;

 Qy 22 VVMTQTPLTLSVTIGQPASISCKSSQSLDSDGKTYLNWLQRPGQSPKRЛИYLVSKLDS 81
 :|:|| |: || |: ||||:||:|| ||||||| ||| | |||: ||||:| |||
 Db 2 IVITQDELSPKVTSGESVSISCRSSKSLLYKDGTЫLNWFQGPQQSPRLLIYLMSTRAS 61

 Qy 82 GVPDRFTGSGSGTDFTLKISRIEAEDLGLYYCWQGTHFPRTFGGGTKLEIK 132
 || |||:|||||:|||:||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
 Db 62 GVSDRFSGSGSGTDFTLIEISRVKAEDVGVYYCQLVEYPLTFGAGTKLELK 112

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